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 WIRELINE  
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Release 2.0 John F. Collins, Biocomputing Research Unit  
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MParch\_nnn n.a. - n.a. database search, using Smith-Waterman algorithm  
 For job Tue Feb 24 23:18:02 1998. Messages: 54, 64, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000, 1010, 1020, 1030, 1040, 1050, 1060, 1070, 1080, 1090, 1100, 1110, 1120, 1130, 1140, 1150, 1160, 1170, 1180, 1190, 1200, 1210, 1220, 1230, 1240, 1250, 1260, 1270, 1280, 1290, 1300, 1310, 1320, 1330, 1340, 1350, 1360, 1370, 1380, 1390, 1400, 1410, 1420, 1430, 1440, 1450, 1460, 1470, 1480, 1490, 1500, 1510, 1520, 1530, 1540, 1550, 1560, 1570, 1580, 1590, 1600, 1610, 1620, 1630, 1640, 1650, 1660, 1670, 1680, 1690, 1700, 1710, 1720, 1730, 1740, 1750, 1760, 1770, 1780, 1790, 1800, 1810, 1820, 1830, 1840, 1850, 1860, 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18730, 18740, 18750, 18760, 18770,

consists of a DNA molecule having two cassettes to express two soluble proteins a heavy chain and a light chain. The vector comprises, operatively linked 5' to 3', a first cassette consisting of the phoA promoter/operator sequences, an *ecori* restriction site, a ribosome binding site (RBS), an *ompA* leader, a *stfI* restriction site, a spacer region, a cloning region bordered by 5' *sacI* and 3' *XbaI* restriction sites, an *NcoI* restriction site between the two cassettes, and a second cassette consisting of an expression control RBS, a *P<sub>elbA</sub>* leader, a human consensus amino terminus spacer region comprising the sequence EWLLLE, a cloning region bordered by 5' *XhoI* and 3' *SpeI* restriction sites followed by a *SfiI* site, expression control stop sequences and a *NotI* restriction site. The *pPho-IT* expression vector contains a light chain stuffer that is 1200 bp in length and a heavy chain stuffer that is 300 bp in length. The nucleotide sequences of the heavy and light chain stuffers encode the heavy and light chain variable domains of a tetanus toxin-specific Fab.

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Db      2674  gccagctcacgcagtctccaggcaccctgtctttgtctccaggggaaagaccctc 2733
        |||||
OY      1  gccagctcacgcagtctccaggcaccctgtctttgtctccaggggaaagaccctc 60

```

Db 4604 gccgagctcaccgagctctccaggcacctgtcttctccaggagggaagagccacc 4663  
|||||  
ov 1 gccgagctcaccgagctctccaggcacctgtcttctccaggagggaagagccacc 60

Db 4664 tctgcaggggccagtcacacagtatttagcaggggcctacttagccttgatacagcagaagacct 4723  

OY 61 TCTGCAGGGCCAGTCACAGTCTTAGCAGCAATACTAGSNTGATACACATGAAGACT 120

Db 4724 ggcaggctccaggctcctctctataggtacatccaggaggccactgcacatcccaaac 4783  
|||||  
V 121 gggcaggctccaggctcctctctataggtacatccaggaggccactgcacatcccaaac 180

Db 4784 aggttcagtgacagtgagggtctggggacagacttcactctacacatcagcagactgaagct 4843  
|||||  
ov 181 AGGTCAGTGCAGTGGCTCTGGCACAGCACTTACTTGGATATGACATATGAGCT 240

4844 gaagattttgagtgactactctgctcagcagctatggttggtcaccctggttcaggcagaagg 4903  
|||||  
241 GAGATTTTGCAGTGTATTTACCTCTCAGCAGTATGCAACACTCTGACCTTCGGTCAGGCG 300  
|||||

Db 4904 accaagggtgaactcaaa 4921  
|||||  
Ov 301 ACCAGCTGGAATCAAA 318

RESULT 3  
ID TL5203 standard; cDNA; 646 bp.  
AC TL5203;  
DT 23-OCT-1996 (first entry)  
DE PC3AP313 anti-tetanus toxoid Ig light chain variable domain cDNA.

DE PCASP13 anti-retroviral coxsack B light chain variable domain CDNA.  
KW Mutagenesis; Ig; immunoglobulin; FR; framework region; variable; CDR;  
KW Complementarity determining region; light; heavy chain; PCR;  
KW polymerase chain reaction; antibody library; diversity; affinity;

KW immunospecificity; ss.  
OS Synthetic.  
PN W09607754-A1.  
PD 14-MAR-1996

PF 01-SEP-1995; U11235.  
PF 02-SEP-1994; US-300386.  
PA (SCRI ) SCRIPPS RES INST.  
PI Barbas CE Buttes CB Lerner BA.

WPI; 96-171625/17.  
 DR Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain  
 PT gene CDR - useful for prodn. of Ig heavy and light chain  
 PT combinatorial antibody libraries

PS Example 1; Page 84; 125pp; English.  
CC T15202 and T15203 are the heavy and light chain variable domains of  
CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a pcomb3

CC are used in an example to demonstrate the prodn. of antibodies for  
CC an antibody library using mutagenic primers. Mutagenic primers of the

100



CC invention have sequences at their 3' and 5' ends both capable of  
 CC binding different framework regions linked by a sequence 6 to 50  
 CC nucleotides long different immunoglobulins produced using the  
 CC primers may be used to produce antibody libraries having diverse and  
 CC novel immunospecificities and affinities. By using mutagenic ONS an  
 CC extremely large population of different randomised binding sites can  
 CC be created and use of the universal light chain increases the number  
 CC of combinations which yield functional heterodimeric antibodies.  
 SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T;

Query Match 81.4%; Score 258; DB 22; Length 646;  
 Best Local Similarity 90 AA; Pred No 9 346-157;  
 Matches 266; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 1 gagctcagcagcttcagcagcaccctcttcttctccaggggaaagagccacctctcc 60  
 QY 4 GAGCTCAGCAGCTTCAGCAGCACCCTCTTCTTCTCCAGGGGAAAGAGCCACCTCTCC 63

Db 61 tgcaggcccaatcacagctgttagcaggggctctttagctgggtaccagcagaaacctgac 120  
 QY 64 TGCAGGCCCAATCACAGCTGTTAGCAGGGGCTCTTTAGCTGGGTACCAGCAGAAACCTGAC 123

Db 121 caagctccaggtctcttcatactatggtatcatcagcagcagcagcagcagcagcagcag 180  
 QY 124 CAGGCTCCAGGCTCTCTCTATCTATGATGATGATGATGATGATGATGATGATGATGAT 183

Db 181 tccagtcagcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240  
 QY 184 TTCAGTCAGCAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 243

Db 241 gattttcagtgactactatcagcagcagcagcagcagcagcagcagcagcagcagcagc 300  
 QY 244 GATTITCAGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303

Db 301 aagctggaactcaaa 315  
 QY 304 AAGGTGGAATCAAA 318

RESULT 4  
 ID Q70487 standard; cDNA; 646 BP.  
 AC Q70487;  
 DT 04-APR-1995 (first entry)  
 DE Anti-tetanus toxoid light chain CDNA from vector, pC3AP313.  
 KW Polymerase chain reaction; primer; mutagenesis; PCR; amplify;  
 KW diversity; antibody; complementarity determining region; CDR;  
 KW framework; constant; light; heavy; phase; immunoglobulin; library; ss.  
 OS Synthetic.  
 FN W03418213-A.  
 PD 18-AUG-1994  
 PF 02-FEB-1994; J01234.  
 PF 02-FEB-1993; US-012556.  
 PF 28-DEC-1993; US-174674.  
 PA (SCR1) SCRIPPS RES INST.  
 PI Barbas CF, Burton DP, Lerner RA.  
 DR WPI: 94-279673/34.  
 PT Oligo-nucleotides - used as PCR primers for producing increased  
 PT diversity antibody libraries, for screening antigens  
 PS Claim 21: Page 84-85; 120pp; English.  
 CC This sequence represents the light chain coding sequence derived from  
 CC the surface display phagemid expression vector, pC3AP313.  
 CC contains the bacteriophage gene III and heavy and light chain variable  
 CC domain sequences for encoding human Fab antibodies against tetanus toxin  
 CC This sequence was pref used in the method of the invention for the  
 CC production of antibody libraries containing increased diversity. The  
 CC sequences given in Q70480-86 are primers which were used for inducing  
 CC mutagenesis in a complementary determining region (CDR) of an  
 CC immunoglobulin light chain gene. These primers contain a 3' terminus  
 CC capable of hybridising to a first framework region, a 5' terminus  
 CC capable of hybridising to a second framework region and a nucleotide  
 CC sequence between the 5' and 3' termini having the formula (NNK)<sub>n</sub>,  
 CC where n is 3-24. These primers may be used to produce antibody  
 CC libraries with increased antibody diversity by inducing mutagenesis

CC within the CDR regions of immunoglobulins heavy or light chains that  
 CC are displayed on the surface of filamentous phage particles comprising  
 CC the library. These primers pref mutate the light chain CDR.  
 SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T;

Query Match 81.4%; Score 258; DB 12; Length 646;  
 Best Local Similarity 90 AA; Pred No 9 346-157;  
 Matches 266; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 1 gagctcagcagcttcagcagcaccctcttcttctccaggggaaagagccacctctcc 60  
 QY 4 GAGCTCAGCAGCTTCAGCAGCACCCTCTTCTTCTCCAGGGGAAAGAGCCACCTCTCC 63

Db 61 tgcaggcccaatcacagctgttagcaggggctctttagctgggtaccagcagaaacctgac 120  
 QY 64 TGCAGGCCCAATCACAGCTGTTAGCAGGGGCTCTTTAGCTGGGTACCAGCAGAAACCTGAC 123

Db 121 caagctccaggtctcttcatactatggtatcatcagcagcagcagcagcagcagcagcag 180  
 QY 124 CAGGCTCCAGGCTCTCTCTATCTATGATGATGATGATGATGATGATGATGATGATGAT 183

Db 181 tccagtcagcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240  
 QY 184 TTCAGTCAGCAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 243

Db 241 gattttcagtgactactatcagcagcagcagcagcagcagcagcagcagcagcagcagc 300  
 QY 244 GATTITCAGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303

Db 301 aagctggaactcaaa 315  
 QY 304 AAGGTGGAATCAAA 318

RESULT 5  
 ID Q49155 standard; cDNA; 387 BP.  
 AC Q49155;  
 DT 01-NOV-1993 (first entry)  
 DE F105 rearranged variable region light chain.  
 KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;  
 KW C104; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;  
 KW chain; epitope; immune deficiency; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..57  
 FT /\*tag= a  
 FT mat\_peptide 58..387  
 FT /\*tag= b  
 FN W09312232-A.  
 PD 24-JUN-1993.  
 PF 10-DEC-1992; U10928.  
 PF 10-DEC-1991; US-804652.  
 PA (DAND) DANA FABER CANCER INST INC.  
 PA (NEWEL) NEW ENGLAND DEACONNESS HOSPITAL CORP.  
 PI Haseltine WA, Marasco WA, Posner MP, Sodroski JG.  
 DR WPI: 93-214174/26.  
 DR P-PSDB: R41286.  
 PT DNA segments encoding monoclonal antibody - which binds to gp120  
 PT and neutralises HIV, for treating AIDS, and for diagnosing and  
 PT monitoring HIV infection  
 PS Claim 1: Page 79; 109pp; English.  
 CC mRNA from the known hybridoma F105 was converted to cDNA and this  
 CC subjected to PCR amplification using primers corresp. to appropriate  
 CC parts of the heavy or light chains and having restriction sites to  
 CC permit cloning. The extension products were isolated and sequenced.  
 CC The recombinant human monoclonal antibody (MAb) binds to a  
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein. It is  
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad  
 CC range of HIV isolates. The MAb may be used to treat immune  
 CC deficiency, esp. at doses of 0.1-10 mg/kg.  
 SQ Sequence 387 BP; 88 A; 111 C; 101 G; 87 T;

Query Match 79.5%; Score 252; DB 7; Length 387;

Best Local Similarity 92.6%; Pred. No. 1.39e-152;  
Matches 289; Conservative 0; Mismatches 20; Indels 3; Gaps 2;

Db 73 acgagctccagaccctctgtttgtctgcaggggaagagaccctctctctgcagg 132  
|||||  
Qy 10 AGCAGTCTCCAGGACCCCTGTCTTCTCTCCAGGGGAAGACACACCTCTCTCTGCGAGG 59  
|||||

Db 133 gccagctcagagtgtagcagcagctacttagcctgtgtaccagcagaaacctggccaggct 192  
|||||  
Qy 70 GCCAGTCAAGACTCTTAGCAGCAATACTTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 129  
|||||

Db 193 cccagctccctcatctatgtgtgctccagcagggccactggcctccagcagaggttcagct 252  
|||||  
Qy 130 CCCAGGCTCTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
|||||

Db 253 ggcagtggtctgggacagacactcactctcaccatcagcagagtgagcctgaagatttt 312  
|||||  
Qy 190 GGCAGTGGCTCTGGACAGACATTCACCTCTCAGCATCAGCAGATGGAGCCTGAGATTTT 249  
|||||

Db 313 gcagtgattactctcagcgaatagtatactccgtttgtacttttggccaggggacccaag 372  
|||||  
Qy 250 GCAGTGATTAATCTGACAGCATATGG-AACACC--TCGACCTTTCGGCCAGGGGACCAAG 306  
|||||

Db 373 ctggagatcaaa 384  
|||||  
Qy 307 GTGGAATCAAA 318  
|||||

RESULT 6  
ID N81537 standard; DNA; 1011 BP.  
AC N81637;  
DT 07-JAN-1991 (first entry)  
DE Anti-pseudomonas aeruginosa human type antibody L-chain coding DNA  
DE contg. constant region of kappa and lambda types  
KW Pseudomonas aeruginosa F4; Pseudomonas aeruginosa HI;  
KW immunotherapy; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT TATA\_signal 264..271  
FT /\*tag= a 325..559  
FT CDS 325..571  
FT /note="P81247"  
FT misc\_feature 572..856  
FT /\*tag= e  
FT /note="L"  
FT CDS 560..895  
FT /\*tag= d  
FT /note="P81245"  
FT misc\_feature 572..856  
FT /\*tag= e  
FT /note="v"  
FT misc\_feature 857..895  
FT /\*tag= f  
FT /note="J"  
FT misc\_feature 572..856  
FT /\*tag= g  
FT /note="Claimed SQ"  
PN J63152984-A.  
PD 25-JUN-1988.  
PE 20-MAR-1987; 064183  
PF 18-AUG-1986; JP-191687  
PA (WAKU-) Wakunaga Seiyaku KK.  
PI WPI: 88-215877/31.  
DR P-PSDB; P81246, P81245.  
PT Anti-pseudomonas aeruginosa type antibody L-chain coding DNA -  
PT contains constant kappa and lambda type regions, and versatile  
PT region recognising pseudomonas F4 and HI types  
PS Disclosure: Pages 610-611; 12pp; Japanese.  
CC It also codes for a variable region recognising Ps.aeruginosa F4 and HI  
CC types. The Ab can be used for immunologic control of infection caused by  
CC Ps.aeruginosa. The antibody is made effective against various classes or

CC subclasses of resistant Ps aeruginosa by recombining corresp DNA L-chain  
CC contg. versatile coding region.  
SQ Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;

Query Match 78.9%; Score 250; DB 1; Length 1011;  
Best Local Similarity 90.3%; Pred No. 3.41e-151;  
Matches 279; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 584 acgagctccagaccctctgtttgtctccaggggaagagaccctctctctgcagg 643  
|||||  
Qy 10 ACCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGACACACCTCTCTCTGCGAGG 59  
|||||

Db 644 gccagctcagagtgtagcagcagctacttagcctgtgtaccagcagaaacctggccaggct 703  
|||||  
Qy 70 GCCAGTCAAGACTCTTAGCAGCAATACTTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 129  
|||||

Db 704 cccagctccctcatctatgtgtgctccagcagggccactggcctccagcagaggttcagct 763  
|||||  
Qy 130 CCAGAGCTCTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
|||||

Db 764 ggcagtggtctgggacagacactcactctcaccatcagcagagtgagcctgaagatttt 823  
|||||  
Qy 190 GGCAGTGGCTCTGGACAGACATTCACCTCTCAGCATCAGCAGATGGAGCCTGAGATTTT 249  
|||||

Db 824 gcagtgattactctcagcgaatagtatactccgtttgtacttttggccaggggacccaag 883  
|||||  
Qy 250 GCAGTGATTAATCTGACAGCATATGG-AACACC--TCGACCTTTCGGCCAGGGGACCAAG 809  
|||||

Db 884 gacatcaaa 892  
|||||  
Qy 310 GAAATCAAA 318  
|||||

RESULT 7  
ID N91359 standard; DNA; 1011 BP.  
AC N91359;  
DT 02-MAR-1990 (first entry)  
DE Anti-P. aeruginosa strain F4 light chain V and J coding regions  
KW Immunoglobulin.  
OS Pseudomonas aeruginosa F4.  
FH Key Location/Qualifiers  
FT CDS 325..372  
FT /\*tag= a 560..895  
FT /\*tag= b  
FT TATA\_signal 264..271  
FT /\*tag= c  
PN J01211498-A.  
PD 24-AUG-1989.  
PF 19-FEB-1988; 035395.  
PR 19-FEB-1988; JP-035395.  
PA (WAKU) Wakunaga Seiyaku KK.  
DR WPI: 89-303485/42.  
DR P-PSDB; P91001.  
PT Production of human IgG monoclonal antibody - by converting human  
PT antibody into other subclasses by genetic engineering  
PS Disclosure: fig. 3; 17pp; Japanese.  
CC This encodes a variable chain and can be connected to a gene encoding  
CC a constant region which determines optional IgG subclass. This can be  
CC used to study subclasses, and as an antigen for prep. IgG1 or IgG3  
CC antibody regions 325-372 connected to 460-571 encode the L chain.  
CC region 572-856 encodes V chain and region 857-895 encodes J chain.  
SQ Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;

Query Match 78.9%; Score 250; DB 1; Length 1011;  
Best Local Similarity 90.3%; Pred. No. 3.41e-151;  
Matches 279; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 584 acgagctccagaccctctgtttgtctccaggggaagagaccctctctctgcagg 643  
|||||  
Qy 10 ACCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGACACACCTCTCTCTGCGAGG 59  
|||||

Db 644 gccagctcagagtgtagcagcagctacttagcctgtgtaccagcagaaacctggccaggct 703  
|||||  
Qy 70 GCCAGTCAAGACTCTTAGCAGCAATACTTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 129  
|||||

Db 704 cccagctccctcatctatgtgtgctccagcagggccactggcctccagcagaggttcagct 763  
|||||  
Qy 130 CCAGAGCTCTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
|||||

Db 764 ggcagtggtctgggacagacactcactctcaccatcagcagagtgagcctgaagatttt 823  
|||||  
Qy 190 GGCAGTGGCTCTGGACAGACATTCACCTCTCAGCATCAGCAGATGGAGCCTGAGATTTT 249  
|||||

Db 824 gcagtgattactctcagcgaatagtatactccgtttgtacttttggccaggggacccaag 883  
|||||  
Qy 250 GCAGTGATTAATCTGACAGCATATGG-AACACC--TCGACCTTTCGGCCAGGGGACCAAG 809  
|||||

Db 884 gacatcaaa 892  
|||||  
Qy 310 GAAATCAAA 318  
|||||

QY 70 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 129  
 Db 704 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 763  
 QY 130 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 189  
 Db 764 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 824  
 QY 140 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 249  
 Db 824 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 883  
 QY 250 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 309  
 Db 884 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 892  
 QY 310 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 318

RESULT 8  
 ID Q44224 standard: DNA: 900 BP.  
 AC Q44224:  
 DT 10-NOV-1994 (first entry)  
 DE Human DNA fragment vk65.8 containing V-kappa gene segment.  
 KW Immunoglobulin; light chain variable region; minilocus;  
 KW isotype switching; unrearranged functional V kappa gene segment;  
 KW human light chain transgene; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT misc\_signal 53..50  
 FT /\*tag= a  
 FT /\*note= "splicing and recombination signal ?"  
 FT exon 116..164  
 FT /\*tag= b  
 FT /\*number= 1  
 FT /\*note= "nucleotides 116-119 represent the  
 FT initiation codon, i.e. the start of the ORF;  
 FT the precise start point of the exon is not  
 FT indicated."  
 FT intron 165..351  
 FT /\*tag= c  
 FT exon 352..550  
 FT /\*tag= d  
 FT /\*note= "ORF not terminated by a stop codon"  
 FT misc\_recomb 553..580  
 FT /\*tag= e  
 FT /\*note= "splicing and recombination signal sequence"  
 PN AC912227-A.  
 PD 24-JUN-1993.  
 PF 17-DEC-1992: US-810279.  
 PR 17-DEC-1991: US-810279.  
 PP 18-MAR-1992: US-853408.  
 PP 23-JUN-1992: US-304068.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N;  
 DR WPI: 93-214169/25.  
 DP P-PSDB: p19650.  
 PT Transgenic non-human animals containing immunoglobulin heavy chain  
 PT trans gene - used to produce useful antibodies by isotype  
 PT switching  
 PS Example 21; Fig 43; 196pp: English.  
 CC The V-kappa specific oligonucleotide Q50327 was used to probe a  
 CC human placental genomic DNA library cloned into pMB13/SP6/T7.  
 CC DNA fragments containing V-kappa segments from positive phase  
 CC clones were subcloned into plasmid vectors. Variable gene segments  
 CC from the resulting clones were sequenced and functional clones were  
 CC selected on the basis of open reading frames, intact donor and  
 CC acceptor splice sites and intact recombination sequences. The  
 CC sequences obtained from four different plasmid clones were  
 CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,  
 CC respectively).  
 SQ Sequence 900 BP: 220 A; 241 C; 201 G; 202 T;

Query Match 77.9% Score 247; DB 7; Length 900;  
 Best Local Similarity 96.2% Pred. No. 4.15e-149;  
 Matches 256; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Db 375 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 434  
 QY 10 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 59  
 Db 435 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 494  
 QY 70 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 129  
 Db 495 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 554  
 QY 130 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 189  
 Db 555 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 614  
 QY 190 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 249  
 Db 615 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 640  
 QY 250 GGCAGTCAAGTCTAGACAGAAATACCTAGTGGTACCAACAAACCTG555TAGGCT 275

RESULT 9  
 ID Q78854 standard: DNA: 900 BP  
 AC Q78854:  
 DT 07-JUN-1995 (first entry)  
 DE Human V-kappa gene vk65.8.  
 KW Transgenic mouse; transgenic animal; antibody engineering;  
 KW variable region; light chain; minilocus transgene;  
 KW chimeric antibody; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 116..650  
 FT /\*tag= a  
 FT intron 163..350  
 FT /\*tag= b  
 FT misc\_signal 653..659  
 FT /\*tag= c  
 FT /\*label= Splicing\_signal  
 FT misc\_signal 672..680  
 FT /\*tag= d  
 FT /\*label= Recombination\_signal  
 PN W09425585-A.  
 PD 10-NOV-1994.  
 PF 25-APR-1994: US-053131.  
 PR 26-APR-1993: US-053131.  
 PP 22-JUL-1993: US-096762.  
 PR 18-NOV-1993: US-155301.  
 PR 03-DEC-1993: US-161739.  
 PP 10-DEC-1993: US-165649.  
 PR 09-MAR-1994: US-209741.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N;  
 DR WPI: 94-358263/44.  
 DP P-PSDB: p62930.  
 PT Transgenic non-human animals producing heterologous or chimeric  
 PT antibodies - for binding a pre-determined human antigen with  
 PT increased affinity  
 PS Disclosure; Fig. 43; 296pp: English.  
 CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in  
 CC Q78852-Q78855, respectively) each contain a V-kappa gene segment  
 CC that can be used to form a complete human light chain minilocus  
 CC transgene for expression in a nonhuman transgenic animal for  
 CC heterologous antibody production. The deduced amino acid  
 CC sequences of the V-kappa coding regions are given in Q62928-Q62931.  
 SQ Sequence 900 BP: 220 A; 241 C; 201 G; 238 T;  
 Query Match 77.9% Score 247; DB 12; Length 900;  
 Best Local Similarity 96.2% Pred. No. 4.15e-149;

Matches 256: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

Db 375 acgagctccagcagccctgtctgtctccagggaagagccaccctctctcagc 434  
 QY 10 AGCGAGTCTCCAGGACCCCTGCTTTGTCCTCAGGGGAAGAGCCACCTCTCTCGAGG 69  
 Db 435 gccagtcagagtggttagcagcagctacttagccttggtaccagcagaacccctgccaggt 494  
 QY 70 GCCAGTCTCAGAGCTTTAGCAGGAAATACCTTAGCTGGTACCAACAGAAACCTGGCCAGGCT 129  
 Db 495 cccagctccctcatgtgtgcatccagcagggccactgagccatccagcagagttcagt 554  
 QY 130 CCCAGGCTCTTATTATGATGATCCAGCAGGCTAGCTGGTATCCAGACAGAGTTTCACT 189  
 Db 555 ggcagtggtgtgtggacagacttccactccaccatccagcagcagctggagcctgaagatttt 614  
 QY 190 GGCAGTGGGCTCTGGACAGACTTCACTCTCAGCATCAGCAGATTGGAGCTTGAAGATTTT 249  
 Db 615 gcagtgattactgtcagcagtatgg 640  
 QY 250 GCAGTGATTACTGTCCAGCAGTATGG 275

RESULT 10  
 ID T37182 standard; DNA: 900 BP.  
 AC T37182;  
 DT 14-APR-1997 (first entry)  
 DE DNA fragment vk65.8, containing variable kappa chain gene.  
 KW Variable; kappa chain; gene segment; human; DNA fragment; vk65.8;  
 KW unearranged; light chain; minilocus; transgene; transgenic; mouse;  
 KW production; heterologous; antibody; gamma; immunoglobulin; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT exon 116..164  
 FT /\*tag= a 352..550  
 FT /\*tag= b  
 PN US5545806-A  
 PD 13-AUG-1996  
 PF 20-AUG-1990: 574748  
 PR 29-AUG-1990: US-574748.  
 PR 31-AUG-1990: US-575962.  
 PR 17-DEC-1991: US-810279.  
 PR 18-MAR-1992: US-853408.  
 PR 23-JUN-1992: US-904068  
 PR 16-DEC-1992: US-990860.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Ionberg N;  
 DR P-PSDB: W03948.  
 DR Prod. of heterologous human immunoglobulin(s) - by immunising transgenic mice  
 PS Example 21; Fig 43: 94pp; English.  
 CC The present sequence is the variable kappa chain gene segment containing human DNA fragment, vk65.8, which was co-injected along with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half CC day mouse embryo pronuclei, to generate an unearranged light chain CC minilocus transgene. The resulting transgenic mice can be used for CC the production of heterologous (i.e. human) antibodies against CC specific antigens, this comprises immunising a mouse with a CC preselected antigen and collecting antigen binding heterologous CC human gamma immunoglobulins.  
 SQ Sequence 900 BP: 220 A; 241 C; 201 G; 238 T;

Query Match 77 98; Score 247; Pos 27; Length 900;  
 Best Local Similarity 96.2%; Pred No 4, 15e-149;  
 Matches 256: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

Db 375 acgagctccagcagccctgtctgtctccagggaagagccaccctctctcagc 434  
 QY 10 AGCGAGTCTCCAGGACCCCTGCTTTGTCCTCAGGGGAAGAGCCACCTCTCTCGAGG 69  
 Db 435 gccagtcagagtggttagcagcagctacttagccttggtaccagcagaacccctgccaggt 494

QY 70 GCCAGTCTCAGAGCTTTAGCAGGAAATACCTTAGCTGGTATCCAGACAGAGTTTCACT 129  
 Db 495 cccagctccctcatgtgtgcatccagcagggccactgagccatccagcagagttcagt 554  
 QY 130 CCCAGGCTCTTATTATGATGATCCAGCAGGCTAGCTGGTATCCAGACAGAGTTTCACT 189  
 Db 555 ggcagtggtgtgtggacagacttccactccaccatccagcagcagctggagcctgaagatttt 614  
 QY 190 GGCAGTGGGCTCTGGACAGACTTCACTCTCAGCATCAGCAGATTGGAGCTTGAAGATTTT 249  
 Db 615 gcagtgattactgtcagcagtatgg 640  
 QY 250 GCAGTGATTACTGTCCAGCAGTATGG 275

RESULT 11  
 ID Q42707 standard; DNA: 390 BP.  
 AC Q42707;  
 DT 01-NOV-1993 (first entry)  
 DE F105VK-F105Jk.  
 KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;  
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;  
 KW chain; epitope; immune deficiency; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /\*tag= a 61..390  
 FT /\*tag= b  
 FT misc\_RNA 1..351  
 FT /\*tag= c  
 FT /\*label= F105VK 352..390  
 FT misc\_RNA  
 FT /\*tag= d  
 FT /\*label= F105Jk 130..165  
 FT misc\_RNA  
 FT /\*tag= e  
 FT /\*label= CDR1 211 231  
 FT misc\_RNA  
 FT /\*tag= f  
 FT /\*label= CDR2 328..354  
 FT misc\_RNA  
 FT /\*tag= g  
 FT /\*label= CDR3 W091222-A.  
 PN W091222-A.  
 PD 24-JUN-1993.  
 PR 10-DEC-1992: U10928.  
 PR 10-DEC-1991: US-804652.  
 PA (DAND ) DANA FARRER CANCER INST INC  
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.  
 PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;  
 DR WPI: 93-214174/26.  
 DR P-PSDB: K38672.  
 DR DNA segments encoding monoclonal antibody - which binds to gp120 PT and neutralises HIV, for treating AIDS, and for diagnosing and PT monitoring HIV infection  
 PS Disclosure: Page 73-74; 109pp; English.  
 CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from CC other F105 VK sequences given elsewhere in the specification) was CC compared with germine gene HumvK325 (Q42706), showing 97.7% CC similarity. By nucleotide sequence analysis, F105 appears to CC be derived from a member of the VK 11 subgroup gene family.  
 SQ Sequence 390 BP: 86 A; 115 C; 102 G; 87 T;

Query Match 77 39; Score 245; DR 7; Length 390;  
 Best Local Similarity 95.9%; Pred No 1 02e-147;  
 Matches 255: Conservative 0: Mismatches 11: Indels 0: Gaps 0:

Db 73 acgagctccagcagccctgtctgtctccagggaagagccaccctctctcagc 132  
 QY 10 AGCGAGTCTCCAGGACCCCTGCTTTGTCCTCAGGGGAAGAGCCACCTCTCTCGAGG 69

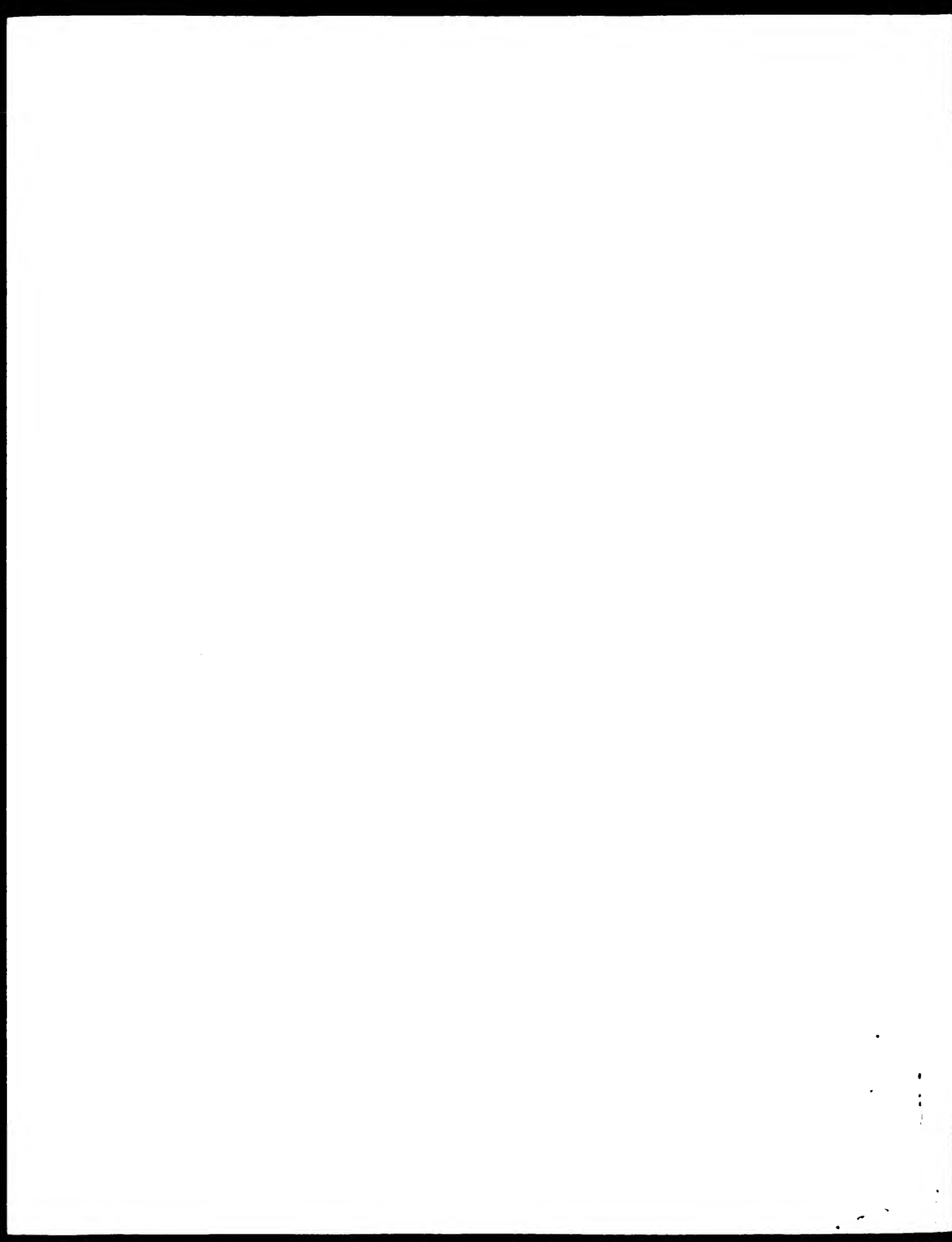




CC then fused with mouse myeloma cell line 653 and the resultant clones  
 CC were screened using Amb a 1 protein. A single cell subclone AL 16-5.2,  
 CC secreting Amb a 1-specific IgG4, kappa antibody was selected. Total  
 CC RNA was prep'd. from the AL 16-5.2 cells and first strand cDNA was  
 CC pred. using oligo dt primers. When the first strand cDNA was used as  
 CC the template, and the 5' and 3' kappa light chain primers (Q66540,  
 CC Q66541) were used in PCR and amplified band of the expected size was  
 CC noted. The DNA sequence of several subclones contg. this amplified  
 CC DNA fragment was determined. The sequence and its deduced AA  
 CC sequence are shown in Q66538 and R56286. Comparison of the deduced  
 CC AL 16-5.2 L-chain sequence with human V region sequences indicates  
 CC that the AL 16-5.2 L-chain is a member of the human VK III subgp.  
 SQ Sequence 325 BP: 79 A: 93 C: 79 G: 74 T:

Query Match 75.18: Score 238: DB 11: Length 325:  
 Rest Local Similarity 90.48: Pred. No. 7.37e-143:  
 Matches 292: Conservative 0: Mismatches 27: Indels 3: Gaps 3:  
 Db 13 acgcadgtccagggcaccctgtcttctcaggggaaagagccaccctctctcaggg 72  
 QY 10 ACGCAGCTCTCCAGGACACCTGTCTTGTCTCCAGGGAAAGAGCCACCTCTCTCGAGG 69  
 Db 73 gccatcagactgttgaagcagcaactacttgccttggtaccagcacaacacctggccaggt 132  
 QY 70 GCCATTCACAGTCTTAGTACGAAATACCTTAGTGTGTAACAAAGAAACCTGGTCAAGCT 129  
 Db 133 ccaggtctctcatctatgtctacatccatcgaaggtcctcctcctccagcagagcttccact 192  
 QY 130 CCGACGGCTCTTATTATGATGCCATCCAGCAGGGGCCACTGGCATCCGACAGAGGTTTCAGT 189  
 Db 193 gccatggggtgtggacacacttccactctccatccagcagcagctggagcctgagagatttt 252  
 QY 190 GGCATGGGCTGTGGACACACTTCCATCTCCATCAATGAGATTCGAGATTTT 249  
 Db 253 gccgtgtattactgtcagcagctttcgttaactcagcagtgagcaggttcggcccaaggagcccaag 312  
 QY 250 GCACTGTATTATCTGACGATGATGG-AAACAC-CTC-3CACTTCTGGCTAGGGAGACCAAG 306  
 Db 313 gttgaaatcaaa 324  
 QY 307 GTGGAAATCAAA 318

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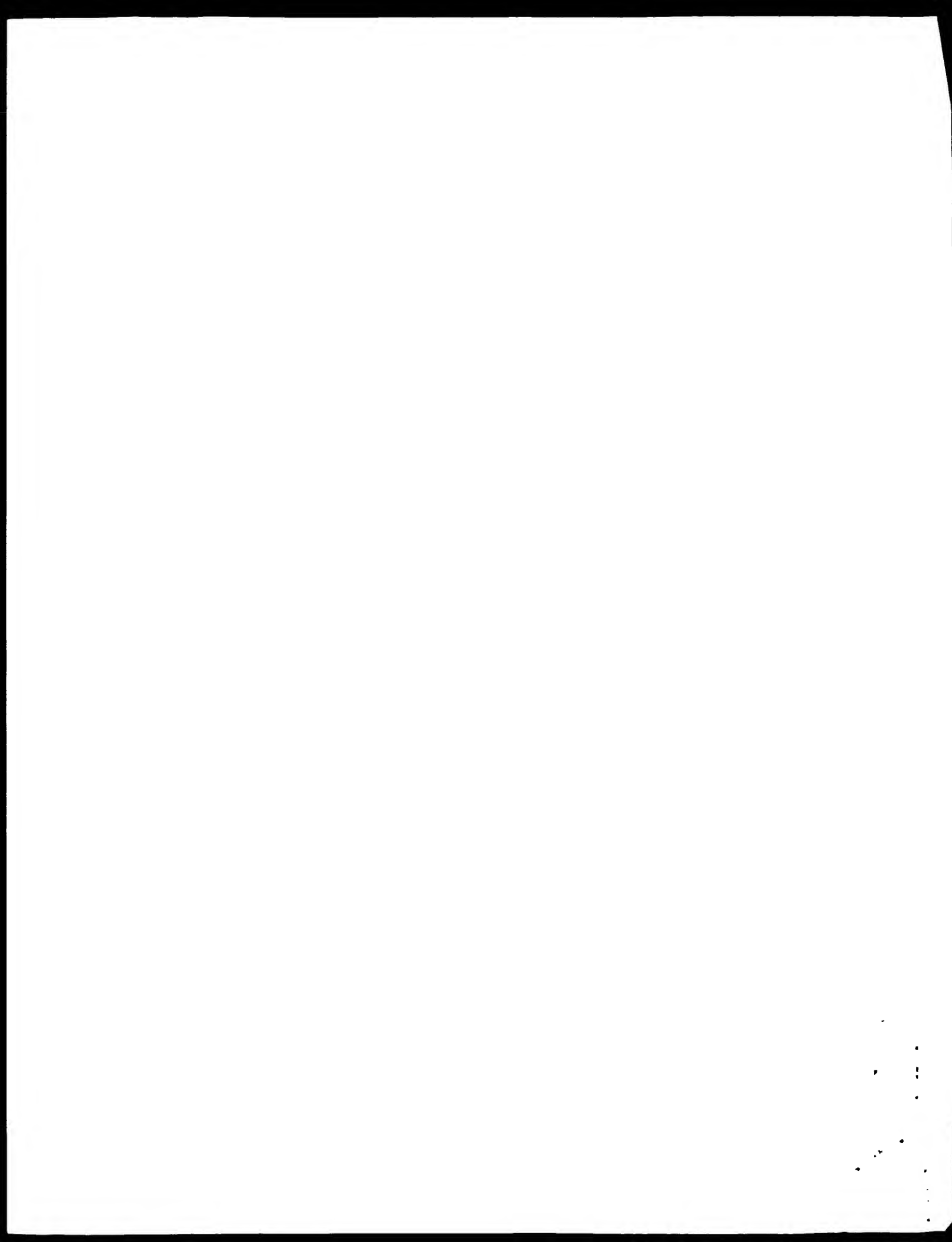


Thu Feb 26 07:04:57 1998

US-08-844-215-20.rstc

Page 9

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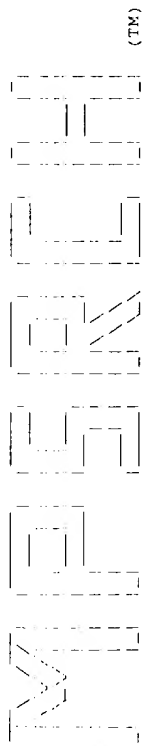
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2	277	87.4	324 98	HMHDPBSAL	Human hepatitis B sur	9.510-224
3	277	87.4	333 95	HS282772	Human anti-HIV-1 gp12	9.510-224
4	264	83.3	330 93	HS17BVL	H.sapiens immunoglob	1.330-211
5	264	83.3	332 99	HUMICKAJ	Human Ig active kappa	1.330-211
6	264	83.3	345 93	HSIM005	H.sapiens mRNA for ka	1.330-211
7	263	83.0	324 99	HMI2LVAE	Human clone SpA31-VL	1.140-210
8	263	83.0	349 98	HMGILIB	Human (clone 1.1) mR	1.140-210
9	262	82.6	324 91	HSIGVK37C	H.sapiens mRNA for Ig	9.790-210
10	262	82.6	402 99	HUMICKAI	Human Ig active kappa	9.790-210
11	262	82.6	402 91	HSIGVKIC	Human mRNA for Ig ka	9.790-210
12	261	82.3	324 95	HS275682	Human rearranged IgM	8.190-208
13	260	82.0	329 91	HSIGRHE19	H.sapiens (RPMR18K) m	7.190-208
14	260	82.0	447 99	HMI2GHA	Human Ig rearranged k	7.190-208
15	259	81.7	312 91	HSIGRHE18	H.sapiens (RPMR18K) m	6.160-207
16	259	81.7	318 91	HSIGRHE20	H.sapiens (RPMR18K) m	6.160-207
17	259	81.7	324 9	HS2EGAL	H.sapiens mRNA for Re	6.160-207
18	258	81.4	324 93	HS2EGAL	H.sapiens mRNA for Re	6.160-207
19	258	81.4	320 99	HMI2KAF	Human Ig rearranged k	6.160-207
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22	258	81.4	320 99	HMI2KAF	Human Ig rearranged k	6.160-207
23	258	81.4	324 94	HS203483	Human clone 2754 Ig k	5.280-206
24	258	81.4	324 91	HSIGVLITD	H.sapiens mRNA for Ig	5.280-206
25	258	81.4	325 99	HUMAB55	Human immunoglobulin	5.280-206
26	258	81.4	339 99	HSABHIV7	H.sapiens mRNA for ka	5.280-206
27	258	81.4	364 99	HMI2L3AC	Human Ig rearranged k	5.280-206
28	258	81.4	387 90	HS20345L	H.sapiens mRNA for an	5.280-206
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30	257	81.1	374 98	HUMFRRP	Homo sapiens rearrang	4.520-205
31	256	80.8	318 99	HUMICKVY2	Human antiplatelet im	3.870-204
32	256	80.8	324 99	HMI2GHA	Homo sapiens immunol	3.870-204
33	256	80.8	390 99	HMI2GHA	Human Ig rearranged k	3.870-204
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35	255	80.4	379 92	HS275682	H.sapiens mRNA for ka	3.870-204
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ALIGNMENTS

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DEFINITION		subgroup III (clone 7F).				
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NID		g514431				
KEYWORDS		autoantibody; Ig J-segment; Ig kappa light chain; Ig subroup III; Ig variable region; immunoglobulin.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.				
AUTHORS		1 (bases 1 to 321) Hexham, J.M., Partridge, L.J., Furmanak, J., Petersen, V.R., Colls, J.C., Peqq, C.A.S., Pees-Smith, B. and Burton, D.K.				
TITLE		Probing the human anti-thyroid peroxidase repertoire of a Hashimoto's thyroiditis patient using combinatorial phage display.				

\*\*\*\*\*



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Distribution rights by IntelliGenetics, Inc.  
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9: HUM2 10: HUM3 11: INV1 12: INV2 13: ORG 14: MAM 15: VFT  
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Statistics: Mean 9.992 Variance 4.477 scale 2.030  
Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.

libraries  
 Unpublished  
 2 (bases 1 to 321)  
 Hexham, J.  
 Direct Submission  
 Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of  
 Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western  
 Bank, Sheffield S10 2UH, UK  
 3 (bases 1 to 321)  
 Hexham, J. M., Furmaniak, J., Pegg, C., Burton, D. P. and Smith, R. P.  
 Cloning of a human autoimmune response: preparation and sequencing  
 of a human anti-thyroglobulin autoantibody using a combinatorial  
 approach  
 Autoimmunity 12 (2), 135-141 (1992)  
 92314301  
 4 (bases 1 to 321)  
 Hexham, J. M., Partridge, L. J., Furmaniak, J., Petersen, V. B.,  
 Colls, J. C., Pegg, C., Rees, Smith, R. and Burton, D. P.  
 Cloning and characterisation of TPO autoantibodies using  
 combinatorial phage display libraries  
 Autoimmunity 17 (3), 157-179 (1994)  
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 1 (bases 1 to 324)  
 Zebadee, S. L., Barbas, C. F. III, Hom, Y.-L., Caethien, P., Graft, R.,  
 Degraw, J., Pyati, J., Lapolla, P., Burton, D. P., Lerner, R. A. and  
 Thornton, G. B.  
 Human combinatorial antibody libraries to hepatitis B surface  
 antigen  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179 (1992)  
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 1 (bases 1 to 333)  
 Ditzel, H. J., Parren, P. W. H. I., Binley, J. M., Sodroski, J., Moore, J. P.,

TITLE Karbas, C.F. and Burton, D.R.  
Mapping the protein surface of human immunodeficiency virus type 1 gp120 using human monoclonal antibodies from phage-display libraries  
J. Mol. Biol. (1997) In press  
JOURNAL 2 (bases 1 to 333)  
REFERENCE Dirzel, H. I., Parren P.W.H.I., Binley, J.M., Sodroski, J., Moore, J.P.,  
AUTHORS Karbas, C.F. and Burton, D.R.  
Direct Submission  
Submitted (20-DEC-1996) Immunology, The Scripps Research Institute,  
JOURNAL 10550 North Torrey Pines Road (IMM2), La Jolla, CA 92037, USA  
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Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 330)  
AUTHORS Chapman, C.J., Spellerberg, M.R., Hamblin, T.J. and Stevenson, F.K.  
TITLE Pattern of usage of the VH4-21 gene by B lymphocytes in a patient  
JOURNAL with PRV infection indicates ongoing mutation and class switching  
Mol. Immunol. 32 (5), 347-353 (1995)  
MEDLINE 95257976

REFERENCE 2 (bases 1 to 330)  
AUTHORS Chapman, C.J.  
TITLE Direct Submission  
JOURNAL Submitted (20-OCT-1994) Caroline J Chapman, Molecular Immunology  
Group, Tenovus Research Laboratory, Southampton University  
Hospitals, Tremona Road, Southampton, SO16 6YU, United Kingdom  
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immunoglobulin-kappa; processed gene.  
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Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 332)  
AUTHORS Kipps, T.J., Tomhave, E., Chen, P. and Fox, P.I.  
TITLE Molecular characterization of a major autoantibody-associated  
JOURNAL cross-reactive idiotype in Sjogren's syndrome  
Immunol. 142, 4261-4268 (1989)  
MEDLINE 89255674  
COMMENT Draft entry and printed copy of sequence kindly submitted by  
T.J. Kipps, 16-AUG-1989.  
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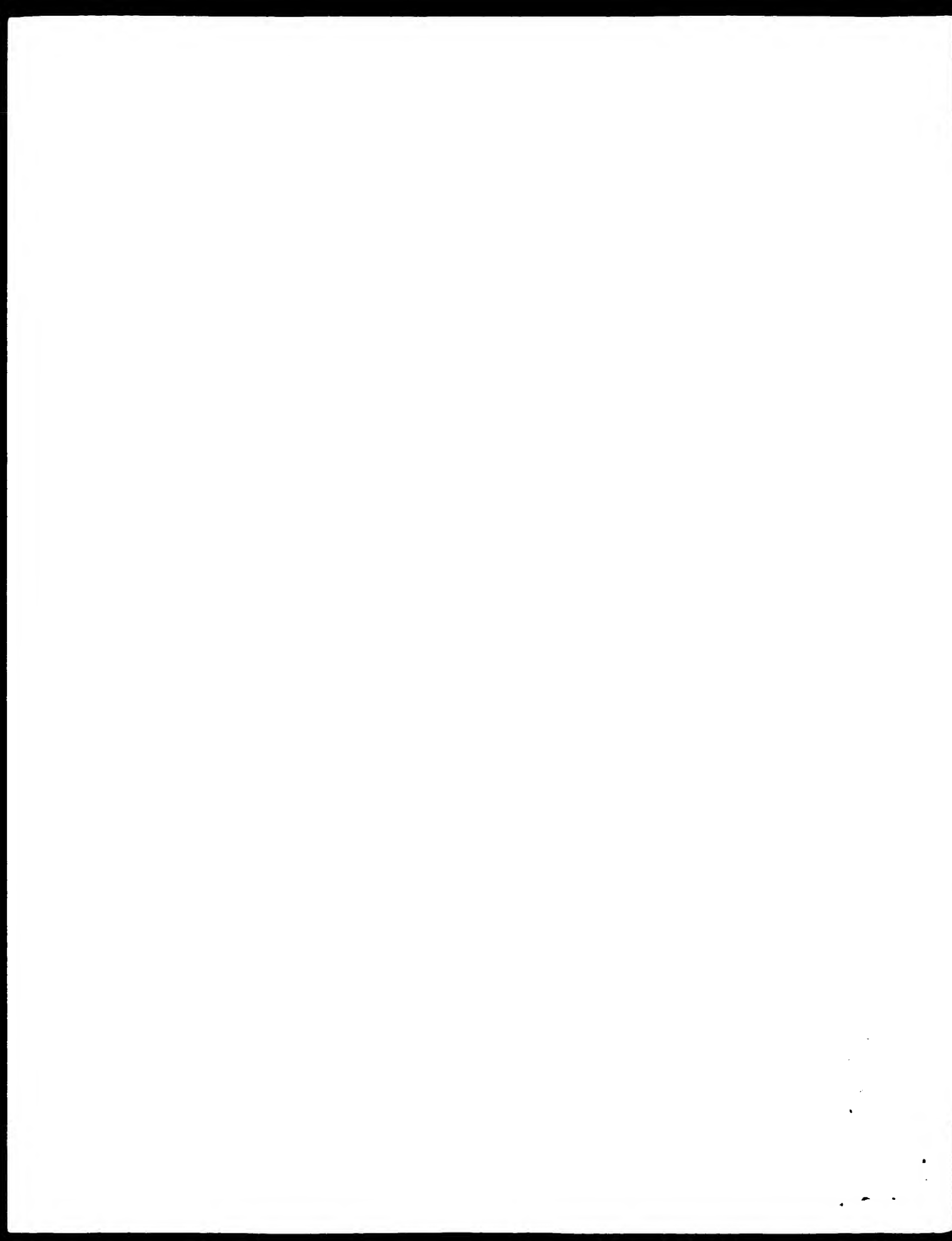


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Job time : 436 secs.





Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280

CONTACT: Kerlavage, AP  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

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Db 205 cccctaagctctgatgtatgtatccatccagtttgcgaagtgagggtccctcagggtca 264  
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Db 325 ttgcaactactactttcagcagagattacagtctctcagaaagttcggccagggaacc 384  
QY 245 TTGCACACTTACTATTGCTCAACAGAGTTTACACACCCCTCGCACTGTCGCACTGTCG 303  
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RESULT 2  
LOCUS AA301261 352 bp mRNA EST 18-APP-1097  
DEFINITION ESF14181 Testis tumor Homo sapiens cDNA 5' end similar to  
immunoglobulin kappa light chain, V region  
ACCESSION AA301261

91953592  
EST.  
human  
SOURCE  
ORGANISM  
Homo sapiens

Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
Homo.

1 (bases 1 to 352)

Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A.,  
Burt, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Goray, T.D.,  
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,  
Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, E., Fine, L.D.,  
Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Georgakilas, N.S.,  
Glodde, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,  
Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, P.,  
Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.,  
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,  
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,  
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,  
Paymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,  
Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,  
Fraser, C.M., and Venter, J.C.  
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based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280

Other ESTs: THC167177

Contact: Kerlavage, AP

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Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

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/organism="Homo sapiens"

/note="Organ: testis; Vector: pBluescript SK-; Site\_1:  
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/sex="male"

/dev\_stage="adult"

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Matches 251; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

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QY 65 GCCGGCAAGTCAGAGTATTAGCAGAGACTTAAATTTGTATCAGCAGAAACCCAGGACAG 124

Db 187 cccctaagctctgatgtatgtatccatccagtttgcgaagtgagggtccctcagggtca 246

QY 125 CCCCAGGCTGTGATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184

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QY 244 TTGCAACTTACATTGTCACAGAGTTACA 274

RESULT 3 AA318377 335 bp mRNA EST 19-APR-1997
LOCUS EST06620 Spleen I Homo sapiens cDNA 5' end similar to
DEFINITION immunoglobulin kappa light chain, V region, anti-thyroglobulin
(GR-X79786)
ACCESSION AA318377
NID q1970863
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 335)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, E., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudex, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F.J.,
Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Olsen, H.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Cline, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018599056
Fax: 3018599423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M3 Reverse.
Location/Qualifiers
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/dev_stage="adult, 23 yrs"
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Best Local Similarity 90.6% Pred No 0.00e+00.
Matches 241. Conservative 0. Mismatches 25. Indels 0. Gaps 0:

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QY 53 TCACATCATTCTGGGGCAATGACAGTAGTAAGAGAGCAATTAATGATGACAGCA 112
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Db 61 aaccagtaagccctaaactctctatctatctatctacatccacttgcgaagtgggtcc 120
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Qy 10 ACCCAGTCTCCATCGGTCCTGTCTGTCTGTGAGAGACAGAGTACCATCATTGGCGG 69

Db 138 gcaagtcagaccattagcaccatttaaatgtgtatcaacaaaacccctgggaagccct 197
Qy 70 GCAAGTCAGAGTATTAGCAGGAACCTTAATTTGGTATCAGCAAGAAACAGAGAGCCCT 129

Db 198 aagctctgtatctatgtgtcatccatttgcaaaactggggtcccatcaaggttcaagtc 257
Qy 130 AAGTCTGTATCTATGCTGTGATCCAGTTTGCAAAGTGGGGTCCCATCGAGGTTTCAGTGGC 189

Db 258 ggtgctctgggacagatttcacatccacatcagcagctctgcaacccctgaggttttaca 317
Qy 190 AGTGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCACCTTGAAGATTTCGA 249

Db 318 acttattactgtcaacagaggttatac 343
Qy 250 ACITACTATTGTCAACAGAGTTACAC 275

RESULT 5 AA361497 357 bp mRNA EST 21-APR-1997
LOCUS EST1040 T-cell lymphoma Homo sapiens cDNA 5' end similar to
DEFINITION Immunoglobulin kappa light chain, V region.
ACCESSION AA361497
NID 92014052
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 357)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, P.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
NATURE 377 (6547 Suppl), 3-174 (1995)
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 95026280
COMMENT Other_ESTs: THC167177
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
7712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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Best Local Similarity 90.8%; Pred. No. 0.00e+00;
Matches 247; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

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Db 133 gcggggcgaagtnagagaatttaaacactatttaaatgtgtatcaacaaaacccaggaag 192
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Db 193 cccctaagctcctctgtatctacggtgtcatccatctgtgcaaaagtgggggtcccatcaagtttc 252
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Qy 184 AGTGGCAGTGGGATGTTGGGACAGATTTCACTCTCAATACATACATAGTATGTTAAGA 242

Db 313 ttgtgcaacttactactgtcacaagaggttaca 344
Qy 243 TTTTCCAACTTACTATTCTCAACAGAGTTTACA 274

RESULT 6 AA295786 382 bp mRNA EST 18-APR-1997
LOCUS EST100987 Pancreas tumor I Homo sapiens cDNA 5' end similar to
DEFINITION similar to immunoglobulin kappa light chain, V region (GR-101279).
ACCESSION AA295786
NID 91948121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 382)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, P.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
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based upon 83 million nucleotides of cDNA sequence
NATURE 377 (6547 Suppl), 3-174 (1995)
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 95026280
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
7712 Medical Center Drive, Rockville, MD 20850 USA

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RESULT      12
LOCUS       AA3300491      282 bp      mPNA          EST          18-APP-1997
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ACCESSION   AA3300491
VERSION     g1952905
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
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Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:
Homo.
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Adams,M D , Kerlavage,A R , Fleischmann,P D., Fuldner,P A ,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georghagen,N.S.,
Glocke,A., Gnehm,C.B., Hanna,M.C., Hedblom,E., Hinkley,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Li,J.-i., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,P.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Pyder,S.E., Scott,J.L., Saudke,D.M., Shirley,P.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,T.M., Gruber,J.J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Madison,P.S., Olson,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Puten,S.M.,
Dillon,P.J., Fannon,M.F., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
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96026280
Other_ESTs: THC167177
Contact: Kerlavage, AR
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Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
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                     /note="Organ: testis; Vector: pBluescript SK-; Site_1-
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BASE COUNT
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Best Local Similarity 92.8%; Pred NO 0.00e+00;
Matches 192; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

dbb 74 agatgaaccagttccattccctctgtatgctatgttaguacagagtgaccatcactt 133
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QY	125	CCCCTAAGTCTCTGATCTATGTGTATCCAGTTTGCRAAGTGGGTCCCATCGAGGTTCA	184		
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Search completed: Tue Feb 24 09:07:30 1998  
 Job time : 129 secs.











CC FILING DATE: 24-MAR-1994  
CC CLASSIFICATION: 530  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M  
CC REGISTRATION NUMBER: 30,223  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 326-2422  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 387 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
CC FEATURE:  
CC NAME/KEY: cDS  
CC LOCATION: 1-387  
CC Sequence 387 BP; 97 A; 107 C; 94 G; 89 T; 0 other;

Query Match 65.1%; Score 207; DB 6; Length 387;  
Best Local Similarity 82.8%; Pred. No. 8,93e-141;  
Matches 250; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Db 74 AGATGACCAAGTCCTGCTGACAGATTTGATCTGATGACAGACAGACATGATGATTT 143  
QY 5 AGCTGACCAAGTCCTGCTGACAGATTTGATCTGATGACAGACAGACATGATGATTT 64  
Db 134 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATGATTT 193  
QY 65 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATGATTT 124  
Db 194 CCGTTAAATCTATGATGATTTGATCTGATGACAGACAGACATGATTTGATGATTT 253  
QY 125 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATGATTT 184  
Db 254 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATGATTT 313  
QY 185 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATGATTT 244  
Db 314 TTGCAACTTATTACTGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATTT 373  
QY 245 TTGCAACTTATTACTGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATTT 304  
Db 374 AGGTGGAAATCAAA 387  
QY 305 AGGTGGAAATCAAA 318

RESULT 7  
ID PCT-US92-09487-74 STANDARD; DNA: UNC; 321 BP.  
AC xxxxxx  
DT 01-JAN-1990

DE Sequence 74, Application PCT/US9209487.  
CC Sequence 74, Application PCT/US9209487  
CC GENERAL INFORMATION:  
CC APPLICANT: Bernhardt, Susan L.  
CC APPLICANT: Better, Marc D.  
CC APPLICANT: Carroll, Stephen F.  
CC APPLICANT: Lane, Julie A.  
CC APPLICANT: Lei, Shau-Ping  
CC TITLE OF INVENTION: Materials Comprising and Methods of  
CC Preparation and Use for Ribosome-Inactivating Proteins

CC NUMBER OF SEQUENCES: 101  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
CC ADDRESSEE: Ricknell  
CC STREET: Two First National Plaza, 20 South Clark  
CC STREET: Street  
CC CITY: Chicago

CC STATE: Illinois  
CC COUNTRY: USA  
CC ZIP: 60603  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent in Release #1 0, Version #1 25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US92/09487  
CC FILING DATE: 19921104  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/901,707  
CC FILING DATE: 19-JUN-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/787,567  
CC FILING DATE: 04-NOV-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Noland, Greta E.  
CC REGISTRATION NUMBER: 35302  
CC REFERENCE/DOCKET NUMBER: 31133  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (312) 346-5750  
CC TELEFAX: (312) 984-9740  
CC TELEX: 25-3856  
CC INFORMATION FOR SEQ ID NO: 74:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 321 base pairs  
CC TYPE: NUCLEIC ACID  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: UNA  
CC Sequence 321 BP; 89 A; 73 C; 77 G; 82 T; 0 other;

Query Match 61.5%; Score 195; DB 10; Length 321;  
Best Local Similarity 80.9%; Pred. No. 2,78e-131;  
Matches 254; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Db 8 AGATGACCTAGCTCCATCTTCCTGCTGCTGATCTGATGACAGACAGACATGATTT 67  
QY 5 AGCTGACCAAGTCCTGCTGACAGATTTGATCTGATGACAGACAGACATGATTT 64  
Db 68 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATTT 127  
QY 65 GCGGGGCGAGTCAGACATTTATGATGATTTGATCTGATGACAGACAGACATTT 124  
Db 128 CTGCTTAAGACCTGATCTGATGATTTGATCTGATGACAGACATTTGATGATTT 187  
QY 125 CTGCTTAAGACCTGATCTGATGATTTGATCTGATGACAGACATTTGATGATTT 184  
Db 188 GTGGGAGTGGATCTGGGACAGATTTATGATGATTTGATCTGATGACAGACATTT 247  
QY 185 GTGGGAGTGGATCTGGGACAGATTTATGATGATTTGATCTGATGACAGACATTT 244  
Db 248 TTGAAATTTATTTATGATGATTTGATCTGATGACAGACATTTGATGATTT 307  
QY 245 TTGAAATTTATTTATGATGATTTGATCTGATGACAGACATTTGATGATTT 304  
Db 308 AGCTTGAATCAAA 321  
QY 305 AGGTGGAAATCAAA 318

RESULT 8  
ID US-08-425-336-72 STANDARD; DNA: UNC; 321 BP.  
AC xxxxxx  
DT 01-JAN-1990

DE Sequence 72, Application US/08425336.  
CC Sequence 72, Application US/08425336  
CC Patent No. 5621083  
CC GENERAL INFORMATION:  
CC APPLICANT: Better, Marc D.

CC APPLICANT: Carroll, Stephen F.  
CC APPLICANT: Studnika, Gary M.  
CC TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
CC TITLE OF INVENTION: Proteins  
CC NUMBER OF SEQUENCES: 140  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
CC STREET: 6300 Sears Tower, 233 South Wacker Drive  
CC CITY: Chicago  
CC STATE: Illinois  
CC COUNTRY: USA  
CC ZIP: 60606-6402  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: Patent In Release #1 0, Version #1 25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/425,336  
CC FILING DATE: 18-APR-1995  
CC CLASSIFICATION: 530  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/064,691  
CC FILING DATE: 12-MAY-1993  
CC APPLICATION NUMBER: US/07/901,707  
CC FILING DATE: 19-JUN-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/787,567  
CC FILING DATE: 04-NOV-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Meyers, Thomas C.  
CC REGISTRATION NUMBER: P-36,989  
CC REFERENCE/DOCKET NUMBER: 31394  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 312/474-5300  
CC TELEFAX: 312/474-0448  
CC TELEX: 25-3856  
CC INFORMATION FOR SEQ ID NO: 72:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 321 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA  
SQ Sequence 321 bp; 89 A; 73 C; 77 G; 82 T; 0 other.

Query Match 61.5%; Score 195; DB 7; Length 321;  
Best Local Similarity 80.9%; Pred. No. 2,78e-141;  
Matches 254; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Db 8 AGATGACGTCCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACTATCACTT 67  
QY 5 AGCTCACCAGTCTCCATGCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACTATCACTT 64  
Db 68 GCGGGGCGAGTCAGACATTAATAGCTATTTAAAGCTGTTCCAGCAGAAAACCGAGGAAG 127  
QY 65 GCGGGGCAAGTCAGAGTATTAGCAGCACTTAAATTTGTTATCAGCAGAAAACCGAGGACAG 124  
Db 128 CTCCTAAGACCTGATCTATCTGTCGCAACAGATTTGGAACTTGGGGTCCCATCAGGTTCA 187  
QY 125 GCGGCAAGGTCGTGATGATGTCGTCATCTGTAGGAGACAGAGTCACTATCACTT 184  
Db 188 GTGGCAGTGGATCTGGGACAGATTATCTCTCAGCATCAGCAGAGCTGCAATATCAAGATT 247  
QY 185 GTGGCAGTGGATCTGGGACAGATTATCTCTCAGCATCAGCAGAGCTGCAATATCAAGATT 244  
Db 248 TTGGAAATTTATTTGTCGAAGATGATGAGCTGCTCCCTGGAGACGTTGGGTGGAGGAGCA 307  
QY 245 TTGCAACTTACTATTGTCGAAGATGATGAGCTGCTCCCTGGAGACGTTGGGTGGAGGAGCA 304  
Db 308 AGCTTCAAAATCAAA 321  
QY 305 AGGTGGAAGTCAAA 318

RESULT 9  
ID US-07-988-430-74 STANDARD; DNA; UNC: 321 BP  
AC XXXXX  
DT 01-JAN-1990  
DE Sequence 74, Application US/07988430.  
CC Sequence 74, Application US/07988430  
CC Patent No. 5416202  
CC GENERAL INFORMATION:  
CC APPLICANT: Bernhardt, Susan L.  
CC APPLICANT: Better, Marc D.  
CC APPLICANT: Carroll, Stephen F.  
CC APPLICANT: Lane, Julie A.  
CC APPLICANT: Lei, Shau-Ping  
CC TITLE OF INVENTION: Materials Comprising and Methods of  
CC TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Prot  
eins  
CC NUMBER OF SEQUENCES: 101  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
CC ADDRESS: Bicknell  
CC STREET: Two First National Plaza, 20 South Clark  
CC STREET: Street  
CC CITY: Chicago  
CC STATE: Illinois  
CC COUNTRY: USA  
CC ZIP: 60603  
CC COMPUTED READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1 0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/988,430  
CC FILING DATE: 19921209  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/901,707  
CC FILING DATE: 19-JUN-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/787,567  
CC FILING DATE: 04-NOV-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: No. 5416202and, Greta E  
CC REGISTRATION NUMBER: 35302  
CC REFERENCE/DOCKET NUMBER: 31133  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (312) 346-5750  
CC TELEFAX: (312) 984-9740  
CC TELEX: 25-3856  
CC INFORMATION FOR SEQ ID NO: 74:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 321 base pairs  
CC TYPE: NUCLEIC ACID  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA  
SQ Sequence 321 bp; 89 A; 73 C; 77 G; 82 T; 0 other;

Query Match 61.5%; Score 195; DB 5; Length 321;  
Best Local Similarity 80.9%; Pred. No. 2,78e-131;  
Matches 254; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Db 8 AGATGACGTCCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACTATCACTT 67  
QY 5 AGCTCACCAGTCTCCATGCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACTATCACTT 64  
Db 68 GCGGGGCGAGTCAGACATTAATAGCTATTTAAAGCTGTTCCAGCAGAAAACCGAGGAAG 127  
QY 65 GCGGGGCAAGTCAGAGTATTAGCAGCACTTAAATTTGTTATCAGCAGAAAACCGAGGACAG 124  
Db 128 CTCCTAAGACCTGATCTATCTGTCGCAACAGATTTGGAACTTGGGGTCCCATCAGGTTCA 187



[illegible]









## RESULT 2

```

QY 302 CCAAGTGGAGTCAAA 318
|||||
RESULT 3
LOCUS p29232 501 bp mRNA EST 25-APR-1995
DEFINITION YesterA v1 Homo sapiens cDNA clone 133862 c1 similar to beta-2-microglobulin
IG KAPPA CHAIN V-1 REGION (HUMAN);
ACCESSION R29232
NID g784367
KEYWORDS EST;
SOURCE human clone-133862 library-Soares placenta Nb2HP vector-pT7T3D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13R1 Psic1-Not I Psic2-Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - 5192(37) primer [5].
AAGTGAAGAAATTCGGGCGAGGAAATTTTTTTTTT 3', double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Hillier, L., Clark, N., Dubuque, J., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Treskiss, E., Waterston, R., Williamson, A., Wohlmann, P., and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 285 1800
Fax: 314 285 1810
Email: est@watson.wustl.edu
High quality sequence steps. 282
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL. Contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Source location/Qualifiers
1..503
/organism="Homo sapiens"
/clone="133862"
BASE COUNT 117 a 122 c 133 g 122 t 9 others
ORIGIN
Query Match 55.2%, Score 175, DB 22, Length 503,
Best Local Similarity 86.2%, Pred No 0.00e+00:
Matches 213: Conservative 0: Mismatches 33: Indels 1: Gaps 1:
Db 5 ungcagacacacattagacacattataaattgatacagcaaaacacaggaagcccc 64
QY 68 GGGCAAGTCACAGATTATTAAGAGAAATTAAATGGATACAGAGAAACAGAGACAGCC 127
|||||
Db 65 ctgaactgctgctatctctgctccatttgcagagtgaggtcccccaggttcagtg 124
|||||
QY 126 ctgaagctctgatctatctgctatctgctatctgctatctgctatctgctatctg 187
|||||
Db 125 cgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 184
|||||
QY 188 cgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 247
|||||
Db 185 cgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 244
|||||
QY 248 cgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 306
|||||
Db 245 atgagag 251
|||||

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QY 307 GTGGAG 313
|||||
RESULT 4
LOCUS T29112 395 bp mRNA EST 26-SEP-1995
DEFINITION EST69384 Homo sapiens cDNA 5' end similar to human fibronectin kappa
light chain V region (AF K12046) (AF13619).
ACCESSION T29112
NID g611210
KEYWORDS EST;
SOURCE human primer-M13 Reverse library-Human Lymphoid tissue.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Superfregii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS Adams, M. D., Kervatage, A. P., Fleischmann, P. D., Feldner, P. A.,
Bult, C. J., Lee, N., Kinkness, E. F., Weinstock, K. G., Gerbacia, J. D.,
White, C. J., Sutton, S., Blake, A., Brand, B. P. C., Chin, M. W.,
Clayton, R. A., Cline, P. T., Cotton, M. D., Earle-Hughes, J., Fine, L. B.,
FitzGerald, L. M., Fitch, W. M., Fritchman, J. D., Geschaden, N. S. M.,
Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, J. P. S.,
Kelley, J. M., Klink, K. M., Kelley, J. C., Liu, J. T., Marra, S. M.,
Merrick, J. M., Moreno-Palacios, P. F., Monaco, D. L., Nguyen, D. T.,
Pellegrino, S. M., Phillips, C. A., Pinder, S. E., Scott, J. L.,
Saudok, D. M., Shirley, B., Small, K. V., Spragg, T. A., Sutcliffe, J. K.,
Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A.,
Coleman, T. A., Collins, E. J., Dimke, D., Feng, P., Ferris, A.,
Fischer, C., Hastings, C. A., He, W. W., Hu, J. S., Greene, J. M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, G., Li, H., Li, H.,
Meissner, P. S., Olsen, H., Paymon, L., Wei, Y. F., Wied, J., Xu, G.,
Yu, G. L., Rubin, S. M., Dillon, P. J., Fannon, M. R., Rosen, C. A.,
Haseitine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)
Other ESTs: EST69383
Contact: Venter, J. C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
FEATURES
Source location/Qualifiers
1..395
/organism="Homo sapiens"
/clone="133862"
BASE COUNT 87 a 110 c 95 g 96 t 7 others
ORIGIN
Query Match 53.0%, Score 168, DB 58, Length 395,
Best Local Similarity 84.5%, Pred No 0.00e+00:
Matches 213: Conservative 0: Mismatches 37: Indels 2: Gaps 2:
Db 70 agttgacacacattagacacattagacacattagacacattagacacattagacacatt 129
|||||
QY 5 AGCTCACCACCTCCATCTCCCTGCTCTGATATGATATGATATGATATGATATGATATGAT 64
|||||
Db 130 gccggcgcagtcagacattagacacattagacacattagacacattagacacattagacac 189
|||||
QY 65 GCGGCGGAGTGGATCTGGGACATTCACATTCACATTCACATTCACATTCACATTCACATTC 124
|||||
Db 190 cccctgaactcctcattcattcattcattcattcattcattcattcattcattcattcatt 249
|||||
QY 125 CCCCCAAGTCTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 184
|||||
Db 250 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 309
|||||
QY 185 GTGGAGTGGATCTGGGACATTCACATTCACATTCACATTCACATTCACATTCACATTCAC 242
|||||

```

Ddb	310	tctcgcgactta	321
QY	243	TTTTCGAACCTTA	254
RESULT	5	T27221	288 bp mRNA EST 06-SEP-1995
LOCUS		EST13641 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V region, rearranged (HT:3785).	
DEFINITION		T27221	
ACCESSION		a609819	
NID		NTD	
KEYWORDS		EST..	
SOURCE		human primer-M13 Reverse library-Human Testis.	
ORGANISM		Homo sapiens	
Eukaryoteae; Metazoa; Eumetazoa; Bilateria; Coelomata;			
Deuterostomia; Chordata, Vertebrata. Gnathostomata, Osteichthyes,			
Sarcopterygii, Chonantia; Tetrapoda; Amniota; Mammalia; Theria;			
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.			
1 (bases 1 to 288)			
ADAMS M.D., Kerlavage A.P., Fleischmann P.D., Feldner P.A.,			
Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,			
White O., Sutton G., Blake J.A., Brandon R.C., Child M.W.,			
Clayton P.A., Cline P.T., Cotton M.D., Earle-Hughes J., Fine L.D.,			
FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,			
Glocke A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr, P.S.,			
Glodek J.M., Klimek K.M., Kelley J.C., Liu L.-I., Marmaros S.T.,			
Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T.,			
Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,			
Saudke D.M., Shirley P., Small K.V., Spriggs T.A., Utterback T.P.,			
Weidman J.F., Li Y., Bednarek D.P., Cao L., Cepeda M.A.,			
Coleman T.A., Collins E.C., Dimke S., Feng F., Ferrie A.,			
Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M.,			
Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,			
Messner P.S., Olsen H., Paymoud L., Wei Y.-F., Wing J., Xu C.,			
Yu G.-L., Puken S.M., Dillon P.J., Fannon M.R., Rosen C.A.,			
Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.			
Initial Assessment of Human Gene Diversity and Expression Patterns			
Based Upon 52 Million Basepairs of cDNA Sequence			
Unpublished (1995)			
Other ESTs: THC24356			
Contact: Venter, JC			
The Institute for Genomic Research			
932 Clopper Rd. Gaithersburg, MD 20878			
Tel: 3018699056			
Fax: 3018699423			
Email: tdbinfo@db.tigr.org			
For clone availability, additional sequence and expression			
information related to this EST, please contact the TIGR Database			
(tdbinfo@db.tigr.org).			
FEATURES			
Source		Location/Qualifiers	
mRNA		/organism="Homo sapiens"	
BASE COUNT	65 a	70 g	67 t 11 others
ORIGIN			
Query Match:		52.7%, Score 167, DB 58, Length 288,	
Best Local Similarity 88.6%;		Pred. No. 0.00e+00;	
Matches 203, Conservative 0; Mismatches 22; Indels 4; Gaps 4;			
Ddb	60	agatgaccagtgntccacgtcgcttcgttgttgcattcttaggcagagagtccacctt	119
QY	5	AGCTCACCGACTGTGCATCGTGCTCTTCTGTGATTGTGGAGACAGAGTACCAC	64
Ddb	120	gccgggcaagtnagacattagcagctattaanttggtatcacgacaagaacagggaag	179
QY	65	CCGGGCCAAGTCAGAGTATTACGACGAACTTAATTGGTATCACGAAAACCCAGGAC	124
Ddb	180	cacctaaagctcctnatcatgctgcgatccagtttgcaagtgggggtcccatacaggtc	239
QY	125	CCCCCAAGCTCGTGCATGTCATGTCATCGATCCAGTTTGCAAGTGGGG-TCCC	183

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LOCUS       T93178             434 bp     mRNA             EST             22-MAR-1995
DEFINITION  Y93909 r1 Homo sapiens cDNA clone 118692 5' similar to gb:U33034
            IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION   T93178
NID         G725091
KEYWORDS    EST.
SOURCE      human c-one-118692 library-Stratagene lung (#937210)
            vector-pBluescript SK+ host-SOUP cells (kanamycin resistant)
            primer-M33p1 Psitel-PCR1 Psitel-2-XhoI Normal lung tissue from a 72
            year old male. Cloned unidirectionally. Primer: Oligo dT. Average
            insert size: 1.0 kb. Uni-ZAP XR Vector; 5' adaptor sequence:
            5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
            5'-CTCGAGTCTTTTCTTTTCTTTT-3'.
ORGANISM    Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 434)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Pohlfinding,T., Tan,F., Trevaskis,F.,
            Waterston,R., Williamson,A., Wohlmann,P. and Wilson,P.
TITLE       WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson PK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 265
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             source
            1..434
            /organism="Homo sapiens"
            /clone="118692"
BASE COUNT   103 a 107 c 103 g 118 t 3 others
ORIGIN
            1 actgcccgggca-gtcaagacattagtattttagctgtatcagcaaaatcaggg 59
            61 ACTTGTGGGGTAAATGACAGATATAGTAAAGATTAAATGGTATACAGAGAAATCAGG 120
            60 aaagccctaaagctccctgatctgtatccatccactttgaacacttgggtcccatcaagg 119
            121 ACAGTCTTAAAGGTCTGTGATCTATGCTGTAATGAGTATGCAAGTGGGTGCTCATGAGG 180
            120 ttcaagggcagtgatcagcagagattcactctcaaatcagcagcagcagcagcagcag 179
            181 TTCAATGGTAAAGTGGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCT 239
            190 aaactatcagcacttactcagcagcagcagcagcagcagcagcagcagcagcagcag 239
            240 AGATTTTGCACACTTATGTTTAAATAGATTAATAGATTAATAGATTAATAGATTAAT 299
            240 ga 241
            300 GA 301
RESULT      8

```

LOCUS	DEFINITION	210 bp	mpna	EST	01-JUN-1995
R69482	YJ83c03.r1 Homo sapiens cDNA clone 15532 5' similar to db:L09085				
	IG KAPPA CHAIN V-I REGION (HUMAN) ;				







of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Euparyotae; Metazoa; Pomeroyae; Bilateria; Coelomata;  
Centrostromia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo;  
1 (bases 1 to 213)

## REFERENCE

Hillier, L., Clark, N., Dubouche, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, B., Rohlfs, J., Soares, M., Tan, F.,  
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and  
Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway Box 8501 St. Louis MO 63109  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 133

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Location/Qualifiers

1..213

/organism="Homo sapiens"

/clone="161395"

51 a 55 c 49 g 55 t 2 others

## BASE COUNT

## ORIGIN

Query Match 34.4%; Score 109; DB 64; Length 213;  
Best Local Similarity 81.9%; Pred. No. 6.46e-179;  
Matches 145; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

Db 1 cccctgaactcttaactatggtggtccgaattacagagtgagggtcccatcaagattca 50  
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QY 125 cccctgaactcttaactatggtggtccgaattacagagtgagggtcccatcaagattca 184  
Db 61 ggggagtgatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 120  
||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 185 ggggagtgatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 243  
Db 121 ttttcaacttattactatcccaadgattacaataactctctataacttttggggcagg 177  
||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 244 ttggcaatttatttggcaatttggcaatttggcaatttggcaatttggcaatttggca 300

Search completed: Tue Feb 24 09:04:59 1998  
Job time : 215 secs.

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Db 134 gccgggcaagtcagagcattgacgactatttaatttggtatcagcagaaaccacgggaaag 193
QY 65 GCGGGCAAGTCAGAGTATTAGCAGGAACCTAAATTTGGTATCAGCACAACCAAGGACAG 124

Db 194 cccctaagctctatctatctatctgcatcccaatttgcaaaagtggggtcccatcaagggtca 253
QY 125 CCCCTAAGCTCTGATCTATCTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 184

Db 254 gtggcagtgatctgggacagatttcactctcaccatcagcagctcgcacactgaaagatt 313
QY 185 GTGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCACCAGTCTGCACCTGAGAGATT 244

Db 314 ttgcaacttactactgtcaacagagatttacagttaccctcagacgttccggccaagggaaca 373
QY 245 TTGCAACTTACTATTGTCAACAGAGATTACAGAACCCCTGGGACGCTTGGGCAAGGGACCA 304

Db 374 aggtggaatcaaa 387
QY 305 AAGTGAAGTCAAA 318

RESULT 2
ID T60117 standard; cDNA; 341 BP.
AC T60117.
DE 15-MAY-1997 (first entry)
KW Antibody; heavy chain; light chain; variable region; human; monoclonal;
KW complementarity determining region; human; adr type hepatitis B virus;
KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine; ss.
OS Homo sapiens.
PN J09020798-A.
PD 21-JAN-1997.
PF 11-JUL-1995; 174752.
PR 11-JUL-1995; JP-174752.
PA (ASAH ) ASAH KASEI KOGYO KK.
DR WPI: 97-140911/13.
PT Human anti-Hepatitis B antibody - used in a adr type HB virus
PT vaccine
PS Claim 7, Page 10-11, 20pp, Japanese.
CC T60116-T60123 represent the coding sequences for the heavy and light
CC chains of the human monoclonal antibody of the invention. The antibody
CC of the invention preferably contains the sequence represented by W13912
CC in the complementarity determining region-1 (CDR-1) of the heavy chain
CC variable region. The antibody of the invention also contains the
CC sequence represented by W13913 in the CDR-3 of the light chain variable
CC region. The antibody is capable of binding to adr type hepatitis B (HB)
CC virus antigen. A human anti-HB virus monoclonal antibody preparation
CC which is highly safe and is effective to adr type HB virus can be
CC provided, using the monoclonal antibody. It can also be used as a
CC vaccine against HB infection.
CC Sequence 341 BP; 80 A; 92 C; 79 G; 80 T;

Query Match 87 1%; Score 276; DP 28; Length 341;
Best Local Similarity 93 7%; Pred No 1.44e-176;
Matches 295; Conservativeness 0; Mismatches 20; Indels 0; Gaps 0;

Db 4 gagatcaaccatctcctctctcctctctctctctctctctctctctctctctctctctct 63
QY 4 GAGCTCACCCAGTCTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63

Db 64 tgcgggcaagtcagagcattgacgactatttaaaacttggtatcagcagaaaccaggga 123
QY 64 TCGCGGGCAAGTCAGAGCATTGACGACTATTAAATTTGGTATCAGTACAGAACTAGGACA 123

Db 124 gccctaagctctatctatctatctatctatctatctatctatctatctatctatctatct 183
QY 124 GCCCTAAGCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 183

Db 184 agtgccagtggtatctgggacagatttcactctcaccatcagcagctcgtcgaacctgaagat 243
QY 184 AGTGCCAGTGGATCTGGGACAGATTTCACCTCTCACCATCACCAGCTCTGCAACCTGAAGAT 243

Db 243 agtgccagtggtatctgggacagatttcactctcaccatcagcagctcgtcgaacctgaagat 243
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Db 244 ttgcaacttactactgtcaacagagatttacagttaccctcagacgttccggccaagggaac 303
QY 244 TTGCAACTTACTATTGTCAACAGAGATTTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303

Db 304 aaggtggaatcaaa 318
QY 304 AAGGTGAAGTCAAA 318

RESULT 3
ID T60119 standard; cDNA; 341 BP.
AC T60119.
DE 15-MAY-1997 (first entry)
KW Antibody; heavy chain; light chain; variable region; human; monoclonal;
KW complementarity determining region; human; adr type hepatitis B virus;
KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine; ss.
OS Homo sapiens.
PN J09020798-A.
PD 21-JAN-1997.
PF 11-JUL-1995; 174752.
PR 11-JUL-1995; JP-174752.
PA (ASAH ) ASAH KASEI KOGYO KK.
DR WPI: 97-140911/13.
PT Human anti-Hepatitis B antibody - used in a adr type HB virus
PT vaccine
PS Claim 8, Page 13, 20pp, Japanese.
CC T60116-T60123 represent the coding sequences for the heavy and light
CC chains of the human monoclonal antibody of the invention. The antibody
CC of the invention preferably contains the sequence represented by W13912
CC in the complementarity determining region-1 (CDR-1) of the heavy chain
CC variable region. The antibody of the invention also contains the
CC sequence represented by W13913 in the CDR-3 of the light chain variable
CC region. The antibody is capable of binding to adr type hepatitis B (HB)
CC virus antigen. A human anti-HB virus monoclonal antibody preparation
CC which is highly safe and is effective to adr type HB virus can be
CC provided, using the monoclonal antibody. It can also be used as a
CC vaccine against HB infection.
CC Sequence 341 BP; 89 A; 88 C; 83 G; 81 T;

Query Match 82 9%; Score 260; DP 28; Length 341;
Best Local Similarity 91 1%; Pred No 5.82e-165;
Matches 287; Conservativeness 0; Mismatches 28; Indels 0; Gaps 0;

Db 4 gaggtgcccagtcacatctcctctctctctctctctctctctctctctctctctctct 63
QY 4 GAGGTCAACCCAGTCTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63

Db 64 tgcgggcaagtcagagcattgacgactatttaaaacttggtatcagcagaaaccaggga 123
QY 64 TCGCGGGCAAGTCAGAGCATTGACGACTATTAAATTTGGTATCAGTACAGAACTAGGACA 123

Db 124 gccctaagctctatctatctatctatctatctatctatctatctatctatctatctatct 183
QY 124 GCCCTAAGCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 183

Db 184 agtgccagtggtatctgggacagatttcactctcaccatcagcagctcgtcgaacctgaagat 243
QY 184 AGTGCCAGTGGATCTGGGACAGATTTCACCTCTCACCATCACCAGCTCTGCAACCTGAAGAT 243

Db 244 ttgcaacttactactgtcaacagagatttacagttaccctcagacgttccggccaagggaac 303
QY 244 TTGCAACTTACTATTGTCAACAGAGATTTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303

Db 304 aaggtggaatcaaa 318
QY 304 AAGGTGAAGTCAAA 318

RESULT 4
ID Q89324 standard; cDNA; 285 BP.
AC Q89324;

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65 GTCGGGTAAGTATTAAGACGAACTTAAATTGGTATCAGCAGCAAAACAGGCAAG 120

128 GGGTAAAGGCTGATATAGTGTGAGTGGCAATAGCAAGGTAAGGATGAGGATTCA 187  
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135 CCCCTAAGGTCCTGATCTATGTGTATGATCAAGTTTCCAAATGGGGTGTATATGAGTTCA 184  
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188 GTGGCGGTGATCTGGAGCAGATTTCACCTCCACATCAACATCAACAGTCTGCAACCTGAGATT 247  
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248 TTGCAACTTACTTCTCAACAGGCTTACAGTACCCCTGGAGCTTCGGCCAGGAGCA 307  
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245 TTGCAACTTACTTCTCAACAGGCTTACAGTACCCCTGGAGCTTCGGCCAGGAGCA 304  
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308 AGGTGGGAATCAAA 321  
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305 AGTGGAGTCAAA 318  
||||| ||||| |||||

RESULT 8

ID T60371 standard; DNA; 324 BP.

AC T60371.

CT 27-Nov-1997 (first entry)

DE Anti-TGF beta-2 scFv antibody 6-HI VL gene.

EE Transforming growth factor beta-2; TGF-beta-2; human;

FF antibody engineering; scFv; phage display; lung fibrosis;

GG arterial injury; proliferative retinopathy; retinal detachment;

HH adult respiratory distress syndrome; liver cirrhosis;

II post myocardial infarction; post-angioplasty restenosis;

JJ scleroderma; vascular disease; cataract; glaucoma; scarring;

KK glomerulonephritis; osteoporosis; immune disease; inflammation;

LL rheumatoid arthritis; macrophage deficiency disease;

MM macrophage pathogen infection, therapy, chain shuffling, ss.

NN Chimeric Homo sapiens;

OO Chimeric synthetic.

PP GB2305921-A.

PN 23-Apr-1997.

PD 07-Oct-1996; 020920.

PE 19-Jan-1996; GB-001081.

PF 06-Oct-1995; GB-020486.

PG (CAMP) CAMBRIDGE ANTIBODY TECHNOLOGY.

PH Bacon L, Green JA, Jackson PH, Johnson KS, Pope AP;

PI Tempest P, Thompson JE, Vaughan TJ, Williams AJ;

PL Wilton AJ;

PM WPI: 97-215360/20.

PN P-FSDB; W15524.

PP Agent contg. antigen-binding domain of human antibody to

PT transforming growth factor beta 1 or 2 - and nucleic acid encoding

PT it, used to neutralise effects of TGF, e.g. for control of fibrosis.

PT Immune and inflammatory disease

PT Example 1; Fig 2b(i); 184pp; English.

CC This DNA sequence comprises the gene encoding the VL domain

CC (W15524) of human scFv antibody 2A-H11 (also known as 6H1), which

CC is specific for transforming growth factor (TGF) beta-2. It was

CC isolated from a light chain shuffle repertoire of a peripheral

CC blood lymphocyte library. The antigen-binding domains of human

CC antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be used

CC to counter the adverse effects of TGF beta, such as (i) promotion

CC of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis,

CC arterial injury, proliferative retinopathy, retinal detachment,

CC adult respiratory distress syndrome, liver cirrhosis, post

CC myocardial infarction, post-angioplasty restenosis, scleroderma,

CC vascular disorders, cataract, glaucoma, or esp. neural scarring and

CC glomerulonephritis, also (not claimed) osteoporosis), or (ii)

CC immune and inflammatory diseases (e.g. rheumatoid arthritis,

CC macrophage deficiency diseases or macrophage pathogen infection).

CC Nucleic acids encoding human antibody VH and VL can be used for

CC prodn. of recombinant antigen-binding domains. These are highly

CC specific, have low dissociation constants (pref. less than 5 nM)

CC and low IC50s for neutralisation.

CC Sequence 324 BP: 90 A: 82 C: 74 G: 78 T:

SO









CC for production of an anti-hepatitis B virus surface antigen antibody by  
 CC ELISA. The MAb's are then purified from large scale cell culture by  
 CC protein A chromatography, size separation on Sephacryl S300 gel and ion  
 CC exchange chromatography on Q-Sepharose. The heavy and light chains of  
 CC the MAb's were isolated and their amino acid sequences determined.  
 CC Primers were generated and used to amplify cDNA synthesised from RNA  
 CC purified from each hybridoma cell line. The sequences of the heavy and  
 CC light chains (nucleic acid and amino acid) from MAb's PEI-1, 2M1-1, 2M1-2  
 CC and MD3-4 are shown in T8538-45 and W24984-91. The MAb's can be used to  
 CC treat HBV infections in immunosuppressed patients or patients with  
 CC chronic active hepatitis, especially liver transplant patients.  
 SQ Sequence 384 BP: 83 A; 108 C; 100 G; 93 T;

Query Match 72.2%; Score 229; DB 33; Length 384;  
 Best Local Similarity 86.3%; Pred. No. 1.56e-142;  
 Matches 271; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Db 68 agatgacccagctccatctccgtgtctgcatctgtgggagacagagtcaccgtcactt 127  
 QY 5 AGCTCACCAGTCTGCATCGTCCCTGCTGTGTGATTTGTNGGACACAGAGTCACCATCACTT 64  
 Db 128 gtggggcaggtcaggtattagcagttggttagcctgtgtatcagcagaaccaggggaag 187  
 QY 65 GCCGGCAAGTCAGAGTATTAGCAGGAACCTAAATTGTATCAGCAGAAACCCAGGGACAG 124  
 Db 188 cccctaaactctgcatctgcatcctcagtttgcagtttgcagagtggtgtcccatcagggttca 247  
 QY 125 CCCCCTAAGGTCTCTGATCTATGTGTCATCCAGTTTGCAAAGTGGGTCCTCATCGAGGTICA 184  
 Db 248 tcggcagtgatctgggacagatttccactctcaccatccaccagcctgcaggctgaagatt 307  
 QY 185 GTGGCAGTGGATCTGGGACAGATTTCACCTTCACCATCACCAGTCTGCAACCTGAAGATT 244  
 Db 308 ttgcaacctactattgtcaacagggtgacagtcctcccttttacttttcggcgaggagacca 367  
 QY 245 TTGCAACTTACTATTGTCAACAGAGTTACACAACCCCTCGGACCTTCGGCCCAAGGGACCA 304  
 Db 368 agdtgaacttcaaa 381  
 QY 305 AGGTGGAAGTCANA 318

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 Job time : 62 secs.

# WATERMAN

Release 2.1D John F. Collins, BioComputing Research Unit  
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Distribution rights by IntelligentGenetics, Inc

MPSrch\_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 08:49:27 1998: MasPar time 136.04 seconds  
889.884 Million cell updates/sec

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N.A. Sequence: 372  
Comp: 1 GAGTCGACGCTCTCTGAGTC  
GAGTCGACGCTCTCTGAGTC

Scoring table: TABLE default  
Gap 6

Nmatch STD DBase 0: Query 0

Searched: 333433 seqs, 126143548 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14  
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Statistics: Mean 9.940 Variance 1.948 Scale 5.112

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	84	21.6	597 24	AA472093	513905 r1 Soares
2	84	21.6	597 23	AA472094	513905 r1 Soares

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C	4	76	20, 4	435	40	AA507475	ab76c05.s1	NCI_CGAP_H	1,18e-08
C	5	34	14, 5	256	34	HS1302358	ab74f07.r1	Soares_mou	3,39e-07
C	6	34	9, 1	230	69	HS1302359	ab74f07.r1	Soares_mou	3,39e-07
C	7	33	8, 9	238	69	HS1300461	aa53401.r1	NCI_CGAP_G	3,46e-21
C	8	33	8, 9	238	55	AA550544	aa53401.r1	NCI_CGAP_G	4,40e-21
C	9	29	7, 8	511	53	HS1358634	aa53401.r1	Soares_mou	4,40e-16
C	10	29	7, 8	511	17	AA464794	aa53401.r1	Soares_mou	4,40e-16
C	11	23	6, 2	255	56	HS1381117	aa53401.r1	Soares_mou	9,95e-07
C	12	23	6, 2	259	30	AA486043	ab12107.r1	Stratagene	9,95e-07
C	13	22	5, 9	156	1	DM36D7S	D. melanogaster	SFS	1,85e-06
C	14	21	5, 6	189	18	AA453361	aa23111.s1	NCI_CGAP_G	3,11e-04
C	15	21	5, 6	189	63	HS1359169	aa23111.s1	NCI_CGAP_G	3,11e-04
C	16	21	5, 6	304	22	AA261024	z116500.s1	NCI_CGAP_G	3,11e-04
C	17	21	5, 6	304	52	HS1377557	z116500.s1	NCI_CGAP_G	3,11e-04
C	18	21	5, 6	400	76	HSAS1414	z143810.r1	Soares_mou	3,11e-04
C	19	21	5, 6	551	40	HS1214338	zw01909.s1	Soares_mou	3,11e-04
C	20	20	5, 4	272	39	AA501612	0917410.s1	NCI_CGAP_L	4,75e-03
C	21	20	5, 4	272	69	HS1397553	0917410.s1	NCI_CGAP_L	4,75e-03
C	22	20	5, 4	354	66	HS1375939	6507307.s1	NCI_CGAP_L	4,75e-03
C	23	20	5, 4	354	32	AA484418	nf07307.s1	NCI_CGAP_L	4,75e-03
C	24	20	5, 4	470	50	HS1454837	z573012.r1	NCI_CGAP_G	4,75e-03
C	25	20	5, 4	540	25	AA515527	z573012.r1	Soares_mou	4,75e-03
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C	29	20	5, 4	597	51	HS1184459	z573012.r1	NCI_CGAP_G	4,75e-03
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C	35	19	5, 1	169	12	HUM6WS574	human chromosome 7	ST	6,39e-02
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C	38	19	5, 1	343	54	HS1206924	z111905.s1	Soares_mou	6,39e-02
C	39	19	5, 1	363	65	HS1273041	z111905.s1	NCI_CGAP_G	6,39e-02
C	40	19	5, 1	410	81	MM1250713	af80h12.r1	Soares_mou	6,39e-02
C	41	19	5, 1	423	70	HS1300938	nh93412.s1	NCI_CGAP_B	6,39e-02
C	42	19	5, 1	442	76	HSAR16248	z582295.r1	Stratagene	6,39e-02
C	43	19	5, 1	524	9	G29434	human	STS	6,39e-02
C	44	19	5, 1	576	34	AA501030	vg04304.r1	Soares_mou	6,39e-02
C	45	19	5, 1	836	42	AA522502	z129305.s1	NCI_CGAP_L	6,39e-02

1

AA472093

597 bp

mpna

EST

18-JUN-1997

LOCUS

vhl0a05.r1 Soares mouse mammary gland BMMG Mus musculus cDNA clone

97524 5' similar to 3' 56761 15 GAMMA 2 chain 2 region (MVAH)

ql\_136438 Mus musculus genome line immunoglobulin gamma constant

region (MOUSE);

ACCESSION

AA472093

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryotae; mitochondrial eukaryotes, Metazoa, Chordata;

AUTHORS

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

TITLE

Murinae; Mus.

JOURNAL

1 (bases 1 to 597)

COMMENT

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouche, J., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, J., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

CONTACT

The WashU-HMI Mouse EST Project

UNPUBLISHED

Unpublished (1996)

CONTACT

Marra M/Mouse EST Project

WASHU-HMI

Mouse EST Project

WASHINGTON

University School of Medicine





```

RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Willie T., Waterston R., Wilson R.;
RT "WashU-Merck EST Project 1997";
RL Unpublished;
CC Contact: Wilton PK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham.
FH Key
FH Location/Qualifiers
FT source
FT 1..266
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker, Site_1, Not I, Site_2, Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5',
FT TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3']
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M.Fatima Bonaldo."
FT /clone_lib="Soares ovary tumor NBHOT"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT mRNA
FT <1..>266
FT Query Match 14.5%; Score 54; DB 54; Length 266;
FT Best Local Similarity 66.5%; Pred. No. 3,39e-57;
FT Matches 119; Conservative 0; Mismatches 59; Indels 1; Gaps 1;
DB 38 agggcagatcaccctgacaggggacagctccacagacacactatcattgggctgagca 97
QY 194 AGGGCGGATTCACCTCTCTCCAGAGACATTCACGACACACCTCTCTCTCTCTCTCTCA 253
DB 98 gctcagatctgagacacgacctgtattactatgagagadctttaccagctcgtcaa 157
QY 254 GCTTGAGCCGAGGACAGAGCTGTCTTATTATGTGGACAGAGGTACTTTTGGATCGA 313
DB 158 tcgcctcagctggtactctgctctctggtggccgtgga-ccttggtcactgtctctctca 215
QY 314 TTAAGGGGGTTTACTACTCTTGAACACTGGGCGGACACCTCTCTCTCTCTCTCA 372
RESULT 6
ID Hs1227079 standard; RNA: EST; 230 BP.
AC AA428970;
NI 92110596;
DT 25-MAY-1997 (Rel 52, Created)
DT 25-MAY-1997 (Rel 52, Last updated, Version 1)
DE sv49b02.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 756939
DE 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria, Primates, Catarrhini, Hominoidea;
RN [1]
RP 1-230
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Willie T., Waterston R., Wilson R.;
RT "WashU-Merck EST Project 1997";
RL Unpublished;
CC Contact: Wilton PK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham.
FH Key
FH Location/Qualifiers
FT source
FT 1..230
FT /organism="Homo sapiens"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker, Site_1, Not I, Site_2, Eco RI; 1st strand cDNA
FT was prepared from human tonsillar cells enriched for
FT germinal center B cells by flow sorting (CD20+, IgD-),
FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
FT primed with a Not I - oligo(dT) primer

```



:



Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estwats@wustl.edu  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information  
Seq primer: -28m3 rev1 ET from Amersham.

## FEATURES

source

1..259  
Location/Qualifiers  
/organism="Homo sapiens"  
/note="Organ: lung; Vector: pBlue-script SK<sup>+</sup>; Site: 1  
Exon: Site\_2; XhoI: Cloned unidirectionally. 1 kb Pst:  
Oligo dT; normal lung. Average insert size: 1.0 kb;  
Uni-TAP XP Vector: 15' adaptor sequence: 5' GAATTCGGACCGAG  
3' -3' adaptor sequence: 5' CTGAGATTTTTTTTTTTT 3'  
/clone="R40613"  
/clone\_lib="Stratagene lung (#937210)"  
/sex="male"  
/rev\_start="72 years"  
/lab\_host="SOLR cells (kanamycin resistant)"  
2..259  
51 a 99 c 71 g 38 t

mRNA

BASE COUNT

ORIGIN

Query Match 6.2%; Score 23; DB 30; Length 259;  
Best Local Similarity 96.0%; Pred No 9.95e-07;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gaaacgctggtcaccgtctctca 25

||||| ||||||| |||||||

QY 348 GGGAACCTCTGTCACCTGTCCTCA 372

RESULT 13

LOCUS

DEFINITION

D. melanogaster STS determined from European Mapping Project

cosmid

ACCESSION

270980

NID

KEYWORDS

sequence tagged site

SOURCE

fruit fly.

ORGANISM

Drosophila melanogaster

Eukaryote; mitochondrial; eukaryotes; Metazoa; Arthropoda;

Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Prosoptilidae; Drosophila

1 (bases 1 to 156)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

STS\_name = Dm35D7S

clone\_name = 36D7

STS\_from\_promoter = SP5

vector\_class = cosmid, Lorist 6

origin\_of\_clone = Oregon-R

in\_situ\_site\_primary = 98C

BLAST\_program = BLASTN

database\_searched = EMBL

database\_version = 45.0 and updates till date\_of\_search

date\_of\_search = 08-01-1995

BLAST\_program = BLASTX

database\_searched = SWISSPROT

database\_version = 32.0

date\_of\_search = 15-12-1995.

Location/Qualifiers

1..156

/organism="Drosophila melanogaster"

/strain="Oregon-P"

/clone="36D7"

BASE COUNT

ORIGIN

28 a 37 c 30 g 27 t 34 others

Query Match

Best Local Similarity

Matches

5; Conservative

2; Mismatches

6; Indels

0; Gaps

0;

Db

22

QY

112

RESULT

LOCUS

DEFINITION

AA465361

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: 41m13 fwd ET from Amersham.

Location/Qualifiers

1..189

/organism="Homo sapiens"

/note="Vector: p771AP Pac (Pharmacia) with a modified

polylinker; Site: 1; Not 1; Site: 2; Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20<sup>+</sup>, IgM<sup>+</sup>).

provided by Dr. Louis M. Staudt (NCI); Dr. David Altman

(NCI) and Dr. Gerald Marti (CREP). cDNA synthesis was

primed with a Not I - Oligo(dT) primer

5'-TGTATCAATTTGAAATGGAGTGGGCGTCATTTTTTTTTTTT-

3'. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p773 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Honalido."

/clone="814100"

/tissue\_type="germinal center B cell"

/lab\_host="DH10B"

complement(1..189)

/db\_xref="GDB:603197"

BASE COUNT

ORIGIN

32 a 59 g 30 t

Query Match

Best Local Similarity

Matches

33; Conservative

0; Mismatches

12; Indels

0; Gaps

0;

Db

119

QY

68

RESULT

LOCUS

DEFINITION

RS1259169

AC

AA465361;

BASE COUNT

ORIGIN

28 a 37 c 30 g 27 t 34 others

DT 19-JUN-1997 (Rel. 52, Last updated, Version 1)  
 DE aa23c11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone 814100 3' similar  
 DE to gb:D90209 DNA-BINDING PROTEIN TAXREB67 (HUMAN);.  
 KW EST.  
 OS Homo sapiens (human)  
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 OC Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP 1-189  
 RA NCI-CGAP;  
 RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 RT Tumor Gene Index";  
 RL Unpublished.  
 CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:  
 CC Robert\_Strausberg@nih.gov This clone is available royalty-free  
 CC through LNL; contact the IMAGE Consortium (info@image.llnl.gov)  
 CC for further information. Seq primer: -41ml3 fwd. ET from Amersham.  
 FH Key Location/Qualifiers  
 FT source 1..189  
 FT /organism="Homo sapiens"  
 FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 FT polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 FT was prepared from human tonsillar cells enriched for  
 FT germinal center B cells by flow sorting (CD20+, IgD-),  
 FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 FT primed with a Not I - oligo(dT) primer  
 FT [5'-TGTTACCAATCTGAAGTGGGCGCGCCTCATTTTTTTTTTTTTTTT-  
 FT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (  
 FT Pharmacia), digested with Not I and cloned into the Not I  
 FT and Eco RI sites of the modified pT7T3 vector. Library was  
 FT through one round of normalization, and was constructed by  
 FT Bento Soares and M. Fatima Bonaldo."  
 FT /clone="814100"  
 FT /clone\_lib="NCI\_CGAP\_GCB1"  
 FT /tissue\_type="germinal center B cell"  
 FT /lab\_host="DH10B"  
 FT complement(<1..>189)  
 FT mRNA  
 SQ Sequence 189 BP; 32 A; 68 C; 59 G; 30 T; 0 other;

Query Match 5.6%, Score 21, DB 63, Length 189,  
 Best Local Similarity 73.3%, Pred. No. 3.13e-04;  
 Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 119 gcacgcgagcgtctcgggacaccccaagcaagaccacgctccc 163  
 |||| ||| |||| |||| || || || |||| ||||  
 Cp 68 GCACGAGGAGAGTCTCAGGGACCTCCCGAGGCTGGCGCCTCCC 24

Search completed: Tue Feb 24 08:51:58 1998  
 Job time : 151 secs.



[illegible]



```

RESULT      5  HUMIGHHC      328 bp      mRNA      PRT      09-NOV-1994
LOCUS       Human Ig rearranged gamma-chain mRNA V-region, partial cds.
ACCESSION  L03164
NID        g185399
KEYWORDS   V-region; immunoglobulin gamma chain; immunoglobulin heavy chain;
SOURCE     Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to
           mRNA.
ORGANISM   Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 328)
AUTHORS   Collet, T A., Poben, P., O'Kennedy, P., Barbas, C.F. III., Burton, D P
           and Lerner, P A
TITLE     A binary plasmid system for shuffling combinatorial antibody
           libraries
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE    93066172
FEATURES   Location/Qualifiers
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               1..328
               /organism="Homo sapiens"
               /cell_type="T-cell"
               /dev_stage="adult"
               /tissue_type="bone marrow"
               /tissue_lib="BMHIV"
               /lab_host="XLI-Blue"
               /map="14q32.33"
             V_region
               1..328
               /partial
               /gene="IGHV#8"
               /note="G00-128-528"
               /codon_start=1
             gene
               1..328
               /gene="IGHV#8"
             CDS
               1..>328
               /gene="IGHV#8"
               /note="This CDS feature is included to show the
               translation of the corresponding V_region. Presently
               translation qualifiers on V_region features are illegal."
               /codon_start=1
               /db_xref="pid:g567158"
               /translation="ELTQSPSSLSASVGRVITTCRASQSISSYLNWYQKPKAPKL
               LIYAASSLSQGVPSRFSGSGSDFTLTISLQPEDFATYVCOGSYSTPTQGGTKL
               EIKRTVA"
BASE COUNT      86 a      88 c      77 g      77 t
ORIGIN
Query Match      86.4%, Score 274, DB 99, Length 328,
Best Local Similarity 93.3%; Pred. No. 2,690-227;
Matches 294; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 1 gaactcaccagtcctccctccctgtctgcatctgtgaggagacagagtcacatcact 60
QY 4 GAGCTCACCAGTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
Db 61 tgcggggaagtcgaagcattgaagcattttaaattggtatcagcagaaaccaggga 120
QY 64 TGCCGGGCAAGTCAGAGTATTAGCAGGAACCTAAATTGGTATCAGCAGAAACCAAGGACA 123
Db 121 gcccttaagctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 180
QY 124 GGCCTTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
Db 181 agtggcagtggtatcgggacatttcaactctcaccatcagcagctctgcaacctgaagat 240
QY 184 AGTGCCAGTGGAATTTGGGACACATTTCTCTCATCTGCTGCTGCTGCTGCTGCTGCT 243
Db 241 ttggcaacttactctgctcaacagaggtttacagtcacccctcagacttttggccaggggacc 300
QY 244 TTGCAACTTACTTATTGTCAACAGAGTATACAAACCCCTCGAGGCTTGGCCAGGAGACC 303

```

```

Db 301 aagctggagatcaaa 315
QY 304 AAGGTGGAGTCAAA 318
RESULT      6  HSC1967OK      346 bp      PNA      PRT      27-FFR-1996
LOCUS       H sapiens rearranged mRNA for polyclonal natural autoantibody
DEFINITION (Igk VJC region)
ACCESSION  X94431
NID        g1208913
KEYWORDS   autoantibody-related; constant region; immunoglobulin;
           immunoglobulin light chain; joining region; kappa chain; variable
           region.
SOURCE     human
ORGANISM   Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 346)
AUTHORS   Eysenbach, G. and Eibel, H.
TITLE     Production and molecular characterization of a monoclonal,
           polyclonal IgM natural autoantibody with rheumatic factor
           activity: A highly cross-reactive natural autoantibody uses
           germline VH and VL segments which are frequently found in
           high-affinity autoantibodies
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 346)
AUTHORS   Eibel, H.
TITLE     Direct Submission
JOURNAL    Submitted (22-DEC-1995) H. Eibel, Klinikum der
           Albert-Ludwigs-Universitaet Freiburg, Klin. Forschergruppe f.
           Rheumatologie, D- 79108 Freiburg, FRG
FEATURES   Location/Qualifiers
             source
               1..346
               /organism="Homo sapiens"
               /isolate="patient EfK with rheumatoid arthritis"
               /sex="female"
               /dev_stage="adult (69 years old)"
               /rearranged
               /tissue_type="peripheral blood B-lymphocytes"
               /cell_type="EBV transformed B-lymphocytes, fused with
               heteromyeloma cell line CB.F7"
               /clone="G1.B6"
               /chromosome="2"
               /notes="PCR primer VK1BACK"
             primer_bind
               1..31
               /note="PCR primer VK1BACK"
             V_segment
               8..293
               /note="V kappa 1 segment, close to germline gene KL 02/012
               (Acc.No. X59315)"
             V_region
               8..329
               /note="rearranged VJ region"
             misc_feature
               81..110
               /note="CDR1 region"
             misc_feature
               156..176
               /note="CDR2 region"
             misc_feature
               273..293
               /note="CDR3 region"
             J_segment
               294..329
               /note="J kappa 1 segment (unmutated)"
             primer_bind
               318..346
               /note="PCR primer HVKFOR"
             C_region
               330..346
               /note="C kappa region"
BASE COUNT      89 a      96 c      82 g      79 t
ORIGIN
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Best Local Similarity 93.3%; Pred. No. 2,450-226;
Matches 293; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 16 agatgaccagctcctccctccctgtctgcatctgtgaggagacagtcacatcact 75
QY 16 agatgaccagctcctccctccctgtctgcatctgtgaggagacagtcacatcact 75

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```

QY 125 CCCCAGGCTGCTATGATGTCATCGATCGATGTAAGAGGGGTCCTCCATGAGGTTCA 184
Db 188 gtgcagtgatctggagagatttactctcaccatccaccatctgcacactgaagatt 247
CY 185 GGGCAGTGGATCGGACAGATTCAGTCTGATCAGTCACTGATGTCAGAACGGAAGATT 244
Db 248 ttcaacttactactcaacaagagttacagttaccctcgaggttttgcgcaggagacca 307
QY 245 TTGAACCTTACTTGTCAACAAGATTAACAACCTGCGGAGATTCGGGCAAGGAGCCA 304
Db 308 agctgagagatcaaa 321
QY 305 AGGTGGAAGTCAAA 318

RESULT 11 HSIGVK110 321 bp PNA PPI 30-MAR-1995
LOCUS H.sapiens mRNA for Ig kappa light chain variable region
DEFINITION (V-J), subgroup I (clone 101).
ACCESSION X73860
NID q516249
KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup I; Ig
variable region; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,
Colls,J.C., Pegg,C., Pees-Smith,R. and Burton,D.R.
TITLE Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Hexham,J.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
Mol. Biology and Biotechnology, P. O. Box 594, Fifth Court, Western
Bank, Sheffield S10 2UH, UK
REFERENCE 3 (bases 1 to 321)
AUTHORS Hexham,J.M., Furmaniak,J., Pegg,C., Burton,D.P. and Smith,R.F.
TITLE Cloning of a human autoimmune response: preparation and sequencing
of a human anti-thyroglobulin autoantibody using a combinatorial
approach
JOURNAL Autoimmunity 12 (2), 135-141 (1992)
MEDLINE 92314301
AUTHORS Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,
Colls,J.C., Pegg,C., Pees-Smith,R. and Burton,D.R.
TITLE Cloning and characterisation of rpo autoantibodies using
combinatorial phage display libraries
JOURNAL Autoimmunity 17 (3), 167-179 (1994)
MEDLINE 95035699
FEATURES Location/Qualifiers
source 1..321
/organism="Homo sapiens"
/isolate="Hashimoto patient"
/note="rearranged"
/sex="female"
/cell_type="thyroid lymphocyte"
/clone_lib="fCmB3 phagemid library"
/clone="101"
V_region 1..321
/note="IgG1/K anti-thyroid peroxidase autoantibody Fab"
/product="Ig kappa light chain variable region, subgroup
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BASE COUNT 86 a 88 c 70 g 77 t
ORIGIN
Query Match 94.5%; Score 268; DB 91; Length 321;
Best Local similarity 92.4%; Pred. No. 1,550-221;

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Matches 291: Conservative 0: Mismatches 24: Indels 0: Gaps 0:
Db 1 gactcaccagctctcactctccctctctctctctctctctctctctctctctctctct 60
CY 4 GAGTTCACCCAGTCTCCATCGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63
Db 61 tgcctggcagctcagacatttagcagctatttaaatctggtatcaccagagagagaaa 120
QY 64 TSCGGGCAAGTCAGAGTATTACGAGGAACCTTAATTTGGTATCAGCAGAAACCCAGGACA 123
Db 121 gccctcaagctctctgctctctctctctctctctctctctctctctctctctctctct 180
QY 124 GCGCCCTAAGGTCCTGATCTATCTGTCATCCAGTTCGCAAGGTCGCTGCTGCTGCTG 183
Db 181 agtcgacgtgagatctgggacagatttctcactctcaccatcagcagctctcaccat 240
QY 184 AGTGGCAGTGGATCTGGGACAGATTCATCTCAGTCCAGTCTGTAACCTTAAAGAT 243
Db 241 ttgcgaacttactactctcagagagatttaccagttaccattcactctcagcctcagag 300
QY 244 TTGCAACCTTACTTGTCAACAAGATTAACAACCTGCGGAGATTCGGGCAAGGAGCCA 303
Db 301 aaagtggatataaa 315
QY 304 AAGGTGGAAGTCAAA 318

RESULT 12 HUMTGHCD 322 bp mRNA PPI 09-NOV-1994
LOCUS Human Ig rearranged gamma-chain mRNA V-region, partial cds.
DEFINITION 103142
ACCESSION L03142
NID q185377
KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to
mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 322)
AUTHORS Collet,T.A., Roben,P., O'Kennedy,P., Barbas,C.F. III, Burton,D.K.
and Lerner,R.A.
TITLE A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10926-10930 (1992)
MEDLINE 93066172
FEATURES Location/Qualifiers
source 1..322
/organism="Homo sapiens"
/cell_type="T-Cell"
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/map="14q32.33"
V_region 1..322
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Db 133 aagctcctgcatatgctgcatccagttgcaaggtgggtggtcccatcaaggttcattggc 192
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RESULT 9 HSX98988 311 bp RNA PPI 17-AUG-1996
LOCUS H sapiens rearranged Ig kappa chain (clone
ACCESSION X98988 121TP5K,131TP7K,131TP8K,131TP15K)
NID g1495650
KEYWORDS immunoglobulin; immunoglobulin kappa chain; immunoglobulin
SOURCE superfamily; joining region; variable region.
ORGANISM human.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 311)
AUTHORS McIntosh,P.S., Asghar,M.S., Kemp,E.H., Watson,P.F., Banga,J.P. and
Weetman,A.P.
TITLE Analysis of Igkappa anti-thyroid peroxidase antibodies from
different tissues from two patients with Hashimoto's thyroiditis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 311)
AUTHORS McIntosh,R.S.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1996) P.S. McIntosh, Univ. of Sheffield, Dept. of
Medicine, Univ. Sheffield Clinical Sciences Centre, Northern General
Hospital, Sheffield S5 7AU, UK
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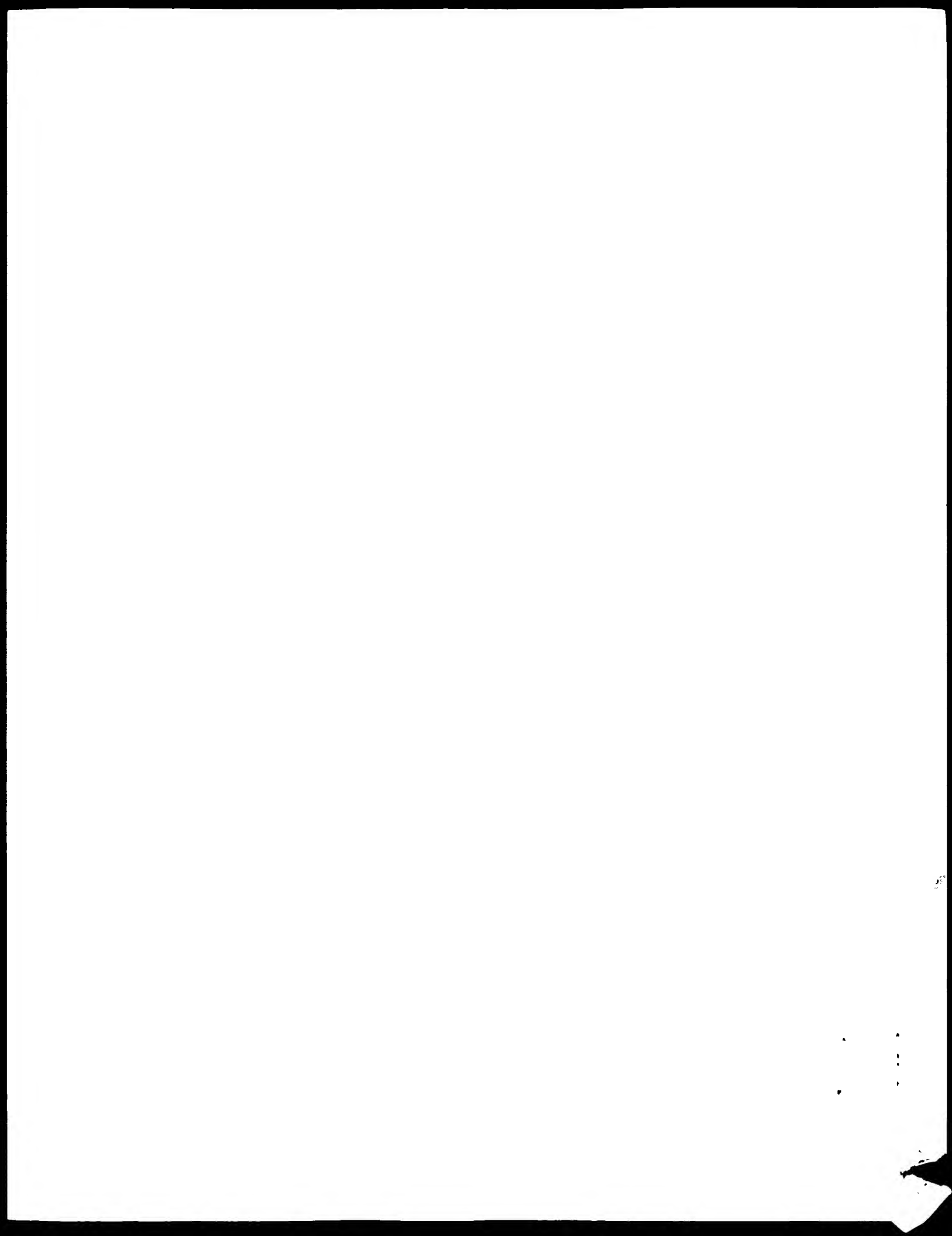
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RESULT 10 HSG039VL 322 bp RNA PRI 27-APR-1995
LOCUS H sapiens mRNA for Ig light chain, variable region (ID:U039VL).
ACCESSION X84343
NID g791023
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SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 322)
AUTHORS Hashimoto,S., Dono,M., Wakai,M., Allen,S.I., Lichtman,S.M.,
Schulman,P., Vinciguerra,V.P., Ferrarini,M., Silver,J., and
Chiorazzi,N.
TITLE Somatic diversification and selection of immunoglobulin heavy and
light chain variable region genes in IgG+ CD5+ chronic lymphocytic
leukemia B cells
JOURNAL J. Exp. Med. 181 (4), 1507-1517 (1995)
MEDLINE 95213674
REFERENCE 2 (bases 1 to 322)
AUTHORS Chiorazzi,N.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-1995) N. Chiorazzi, North Shore University
Hospital, Cornell University Medical College, 300 Community Drive,
Manhasset, New York 11030, USA
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 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
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 REFERENCE 1 (bases 1 to 294)  
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., Bult, C.J., Sutton, G., Blake, J.A., Brannon, P.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, J.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodde, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.P., Weidman, I.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@igir.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.  
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 DEFINITION r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 752524  
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(HUMAN);  
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 REFERENCE 1 (bases 1 to 379)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Post, S., Kuraba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, J., Waterston, R., and Wilson, R.  
 TITLE WashU-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 This clone is available royalty-free through HMI: contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 361.  
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 QY 113 GCGAGGCTCCAGGAGAGGGGCTGGAGTGGGTGGGTCGTATATGTTGATGGAGTAATTC 172  
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 QY 293 CAGA 296







NUM	ORGANISM	REFERENCE	TITLE
92030551	Human.	Adams,M.D., Kerlavage A.P., Fleischmann, R.P., Feldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, C., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, J.B., Cotton, M.D., Earle-Hughes, J., Fink, J.L., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Goodhead, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedbloom, E., Hinkley, P.S., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmorek, S., McKee, S.L., Morrell-Palant, P., McDonald, L.A., Nguyen, T.J., Pellegrino, S.J., Phillips, C.A., Ryder, S.E., Scott, J.I., Sandak, D.M., Shirley, R., Small, K.V., Spriggs, J.A., Unterbach, T.P., Weidman, I.F., Wiley, D., Zerkow, D., Zeng, D.-F., Zeng, A., Zerkow, C., Hastings, G.A., Dunke, D., Peng, D.-F., Perle, A., Fischer, C., Hastings, G.A., He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hung, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, P., Xu, C., Yu, G.L., Rubin, S.M., Dillond, P.J., Fannon, M.P., Posen, C.A., Hasegawa, W.A., Fields, C.	Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence
96026380	Human.	Fraser, C.M. and Venter, J.C.	Nature 377 (6547 Suppl). 3-174 (1995)

Contact: Kerlavage, AP  
Bioinformatics for Genomic Research  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: [arkerlav@tigr.org](mailto:arkerlav@tigr.org)  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tghdb/hgi/hgi.html>)

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ACCESSION	AA360195					
RID	7201273					



ACCESSION AA000945  
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 SOURCE human.  
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 Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.  
 REFERENCE 1 (bases 1 to 304)  
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.P., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geodhagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palances, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, P.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Korak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT Other ESTs: THC80285  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018599056  
 Fax: 3018599423  
 Email: arkerlavage@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)  
 Seq primer: M13 Reverse.  
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 QY 122 CAGGTAAGGGGTGGAGTGG 141















COMMENT

Unpublished (1995)

Contact: Wilson PK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

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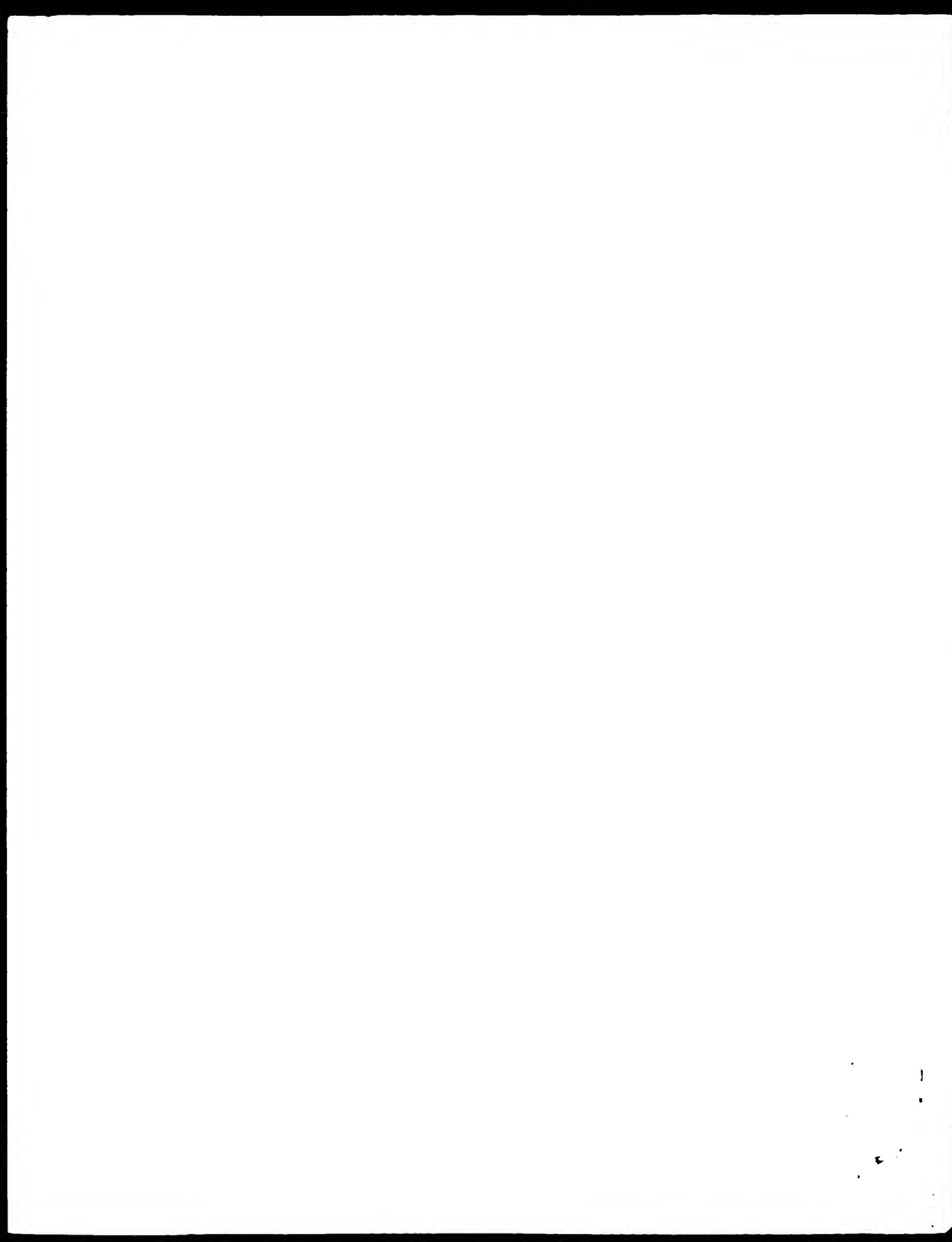
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CC FILING DATE: 31-OCT-1986  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 06/904,517  
CC FILING DATE: 05-SEP-1986  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-50-7  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 576-0300  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 423 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
CC ORGANISM: Homo sapiens  
CC CELL TYPE: Hybridoma  
CC CELL LINE: PEI-1  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..423  
CC Sequence 423 BP; 87 A; 100 C; 131 G; 105 T; 0 other:  
  
Query Match 66.4%; Score 247; DB 6; Length 423;  
Best Local Similarity 90.8%; Pred. No. 1.35e-167;  
Matches 275; Conservative 0; Mismatches 28; Indels 3; Gaps 0,  
  
Db 59 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 118  
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 61  
  
Db 119 CTGTGGCAGCGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 178  
Qy 62 CTGTGGCAGCGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 121  
  
Db 179 CAGGCAAGGGGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 238  
Qy 122 CAGGCAAGGGGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 181  
  
Db 239 CAGATCTGGTGAAGGGGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 298  
Qy 182 CAGATCTGGTGAAGGGGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 241  
  
Db 299 TGCAATATCAGCGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 358  
Qy 242 TGCAATATCAGCGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 301  
  
Db 359 TTT 361  
Qy 302 TTT 304

CC STREET: Two Embarcadero Center, Eighth Floor  
CC CITY: San Francisco  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 94111-3834  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/458,671  
CC FILING DATE: 06-JUN-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/259,372  
CC FILING DATE: 14-JUN-1994  
CC APPLICATION NUMBER: US 07/871,426  
CC FILING DATE: 21-APR-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/676,036  
CC FILING DATE: 27-MAR-1991  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/538,796  
CC FILING DATE: 15-JUN-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/192,754  
CC FILING DATE: 11-MAY-1988  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 06/925,196  
CC FILING DATE: 31-OCT-1986  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 06/904,517  
CC FILING DATE: 05-SEP-1986  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-50-7  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 576-0300  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 423 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
CC ORGANISM: Homo sapiens  
CC CELL TYPE: Hybridoma  
CC CELL LINE: PEI-1  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..423  
CC Sequence 423 BP; 87 A; 100 C; 131 G; 105 T; 0 other:  
  
Query Match 66.4%; Score 247; DB 7; Length 423;  
Best Local Similarity 90.8%; Pred. No. 1.35e-167;  
Matches 275; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
  
Db 59 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 118  
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 61  
  
Db 119 CTGTGGCAGCGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 178  
Qy 62 CTGTGGCAGCGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 121  
  
Db 179 CAGGCAAGGGGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 238  
Qy 122 CAGGCAAGGGGCTGGTGGAGTCTGGGGAGCGGTGGTCAGCGCTGGGAGGTGCTCGAGACTCT 181





CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 455-5100  
CC TELEFAX: (619) 455-5110  
CC INFORMATION FOR SEQ ID NO: 47:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 294 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC IMMEDIATE SOURCE:  
CC CLONE: VR25C  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..294  
SQ Sequence 294 BP: 53 A: 71 C: 96 G: 64 T: 0 other:  
  
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Best Local Similarity 85.6% Pred No 1.98e-137:  
Matches 250: Conservative 0: Mismatches 42: Indels 0: Gaps 0:  
  
Db 1 GAGGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 60  
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QY 1 GAGGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 60  
  
Db 61 TCGTGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 120  
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QY 61 TCGTGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 120  
  
Db 121 CCAGGCAAGGCGGTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 180  
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QY 121 CCAGGCAAGGCGGTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 180  
  
Db 181 GAGAGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 240  
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QY 181 GAGAGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 240  
  
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QY 241 CTGCAATGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 300  
  
RESULT 7  
ID PC/US93-10555-4: STANDARD: DNA: UNC: 345 BP  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 41: Application PC/TUS9310555  
CC Sequence 41: Application PC/TUS9310555  
CC GENERAL INFORMATION:  
CC APPLICANT: SILVERMAN, GREGG J.  
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES  
THROUGH  
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA  
TES  
CC TITLE OF INVENTION: THEREOF  
CC NUMBER OF SEQUENCES: 51  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Spensley Horn Jubas & Lubitz  
CC STREET: 1880 Century Park East - Suite 500  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PC/TUS93/10555  
CC FILING DATE: 29-OCT-1993  
CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Howells, Stacy L.  
CC REGISTRATION NUMBER: 34,842  
CC REFERENCE/DOCKET NUMBER: PD-2630  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 455-5100  
CC TELEFAX: (619) 455-5110  
CC INFORMATION FOR SEQ ID NO: 41:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 345 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC IMMEDIATE SOURCE:  
CC CLONE: SpA1-29  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..345  
SQ Sequence 345 BP: 74 A: 88 C: 108 G: 75 T: 0 other:  
  
Query Match 55.4% Score 206: DB 11: Length 345:  
Best Local Similarity 85.8% Pred No 6.54e-136:  
Matches 247: Conservative 0: Mismatches 41: Indels 0: Gaps 0:  
  
Db 2 AGGTAAATGCTGGAGCTTGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 60  
|||||  
QY 2 AGGTAAATGCTGGAGCTTGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 60  
  
Db 62 CTGCTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 120  
|||||  
QY 62 CTGCTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 120  
  
Db 122 CCAGGCAAGGCGGTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 180  
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QY 122 CCAGGCAAGGCGGTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 180  
  
Db 182 GAGAGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 240  
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QY 182 GAGAGTGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 240  
  
Db 242 TGCAGATGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 300  
|||||  
QY 242 TGCAGATGCAGCTTTGGAGTCTGCGGGAGAGCTTGGTACAGAGCTGGGGGGTGGTGGAGACTC 300  
  
RESULT 8  
ID PC/US93-10555-4: STANDARD: DNA: UNC: 372 BP  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 43: Application PC/TUS9310555  
CC Sequence 43: Application PC/TUS9310555  
CC GENERAL INFORMATION:  
CC APPLICANT: SILVERMAN, GREGG J.  
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES  
THROUGH  
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA  
TES  
CC TITLE OF INVENTION: THEREOF  
CC NUMBER OF SEQUENCES: 51  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Spensley Horn Jubas & Lubitz  
CC STREET: 1880 Century Park East - Suite 500  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25











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CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: SpA3-37
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..360
CC Sequence 360 BP; 75 A, 96 C, 111 G, 78 T, 0 other;

Query Match      52.2%  Score 194; DB 11; Length 360;
Best Local Similarity 83.4%; Pred. No. 1.12e-126;
Matches 242; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Db      2 AGGTAAAGCTGCTCGAGTCTGGGGAGAGATTGGTATAGAGCTTGGGGGTCCTCGAGACTCT 61
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QY      2 AGGTCCAGTGTGCTCGAGTCTGGGGAGAGGCTGGTCCAGGCTGGGAGGCTCCCTGAGACTCT 61
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      62 CTTGTGACGCTCTGGATTTCACCTTTAGCAGCCCATGCCATGAGCTGGGTCCGCCAGGCTC 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      62 CTTGTGACGCTCTGGATTTCACCTTTAGCAGCTGCTTATGGCATGCACCTGGGTCCGCCAGGCTC 121
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      122 CAGGGAGGGGCGCTGGAGTGGGTCTCAGATATTAGTCCAGTGGTGTAGCACATATTATG 181
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      122 CAGGCAGGGGCTGGAGTGGGTGGCAGGTATATGTTTGTGGAAGTAATCAATACTATT 181
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      182 CAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGACAATTCAGAGACACGCTGTATT 241
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      182 CAGACTCCGTGAAGGGGCTGATTACAGCTCTCCAGAGACAATTCAGAGACACGCTGTATT 241
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      242 TGCATATGAACACCTGAGAGCCGAGACACGCGCTTATTACTGTGCG 291
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      242 TGCATATGAACACCTGAGAGCCGAGACACGCGCTTATTACTGTGCG 291
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Search completed: Tue Feb 24 14:30:27 1998  
Job time : 60 secs.

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(MI)

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Distribution rights by Intelligentics, Inc.

MPSPrch\_no      Prch.      Prch. database      Prch. using Smith-Waterman algorithm

Run: 00  
 Tue Feb 24 09:40:37 1988: Maspar time 62.05 Seconds  
 691 824 Million cell updates/sec  
 Tabular output not generated.

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>US-08-844-215-19
Description:
(1,372) from US08844215.seq
Perfect Score: 372
1 GAGGTGACAGCTGCTGTCACCTC
CTGACCTTCTGACAGGCTGAC
Comp:
CCCTGCTACCGGCTCTCTCA 372
GGATACAGCTGACAGGCTGCT

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Scoring table: TABLE default  
Gap 6

Nmatch

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-qeneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.102; Variance 4.826; scale 1.679

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Pred. No.
1	253	70.7	583	13	Q78971	Human immunoglobulin	5.69e-163
2	257	69.1	345	31	T60362	Anti-TGF beta-2 scFv	1.01e-158
3	257	69.1	512	13	Q78968	Human immunoglobulin	1.01e-158
4	253	68.0	345	31	T60380	Anti-TGF beta-1 scFv	6.82e-156
5	250	65.2	269	33	T60381	Anti-TGF beta-1 scFv	9.24e-154
6	249	64.9	1521	2	G11180	Protein heavy chain	4.55e-153
7	247	66.4	423	33	T85838	Monoclonal antibody P	1.15e-151
8	247	66.4	423	33	T46328	Monoclonal antibody P	1.15e-151
9	247	66.4	423	10	Q4572	Sequence of the V H Fc	1.15e-151
10	247	66.4	333	37	Q4572	Sequence encoding the	1.15e-151
11	246	66.1	336	2	Q11472	Anti-human Ptd HAM-2	6.08e-151
12	245	65.9	339	2	Q11956	Anti-human Ptd REC-A	3.10e-150
13	242	65.1	309	33	T50392	Anti-TGF beta-1 scFv	4.09e-148
14	240	64.5	357	28	T50372	Coding sequence for P	1.06e-146
15	239	64.0	350	25	T50370	Anti-TGF beta-1 scFv	2.70e-145

CC into E.coli 490A. The fragments were then subcloned by colony  
 CC hybridisation. The Vh genes and the DNA fragments encoding them are  
 CC useful in producing human immunoglobulin in mammalian hosts.  
 SQ Sequence 583 BP; 136 A; 127 C; 186 G; 134 T;  
 Query Match 70.7%; Score 263; DB 13; Length 583;  
 Best Local Similarity 94.8%; Pred. No. 5,69e-16;  
 Matches 279; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 Db 180 aggtacagctggtggagctggtggagcgtgtccagcctggaggtccctgagactct 239  
 QY 2 AGGTGACAGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 61  
 Db 240 cctgtgacagctggtggagctggtggagcgtgtccagcctggaggtccctgagactct 299  
 QY 62 CCGTGTGAGGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 121  
 Db 300 cagcgaagcgtggtggagctggtggagcgtgtccagcctggaggtccctgagactctg 359  
 QY 122 CAGGCAAGGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 181  
 Db 360 cagcgtccgagcgtggtggagctggtggagcgtgtccagcctggaggtccctgagactct 419  
 QY 182 CAGCACTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 241  
 Db 420 tgcacatgaacagcgtggtggagctggtggagcgtgtccagcctggaggtccctgagactct 474  
 QY 242 TGCACATGAACAGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 296  
 RESULT 2  
 ID T60369 standard; DNA; 345 BP.  
 AC T60369; 1997 (first entry)  
 DE Anti-TGF beta-2 scfv antibody 2A-H11 Vh gene.  
 KW Transforming growth factor beta-2; TGF-beta-2; human;  
 KW antibody engineering; scfv; phage display; lung fibrosis;  
 KW arterial injury; proliferative retinopathy; retinal detachment;  
 KW adult respiratory distress syndrome; liver cirrhosis;  
 KW post myocardial infarction; post-angioplasty restenosis;  
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;  
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;  
 KW rheumatoid arthritis; macrophage deficiency disease;  
 KW macrophage pathogen infection; therapy; ss.  
 OS Chimeric Homo sapiens;  
 OS Chimeric synthetic.  
 PN GB230521-A.  
 PD 23-APR-1997.  
 PF 07-OCT-1996; 020920.  
 PR 19-JAN-1996; GB-001081.  
 PR 06-OCT-1995; GB-020486.  
 PA (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Bacon L., Green JA, Jackson RH, Johnson KS, Pope AR;  
 PI Tempest PP, Thompson JE, Vaughan TJ, Williams AJ;  
 PI Wilton AJ;  
 DR WPI: 97-215160/20  
 DR p-PSDB: W15522.  
 PT Agent contg. antigen-binding domain of human antibody to  
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding  
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,  
 PT immune and inflammatory disease  
 PS Example 1; Fig 2a(i); 184pp; English.  
 CC This DNA sequence comprises the gene encoding the Vh domain  
 CC (W15522) of human scfv antibody 2A-H11 (also known as 6H1), which  
 CC is specific for transforming growth factor (TGF) beta-2. It was  
 CC isolated by panning a phage antibody library produced from cloned  
 CC germline V genes and synthetic CD8s. The antigen-binding domains  
 CC of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can  
 CC be used to counter the adverse effects of TGF beta, such as (i)  
 CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung  
 CC fibrosis, arterial injury, proliferative retinopathy, retinal  
 CC detachment, adult respiratory distress syndrome, liver cirrhosis,  
 CC post myocardial infarction, post-angioplasty restenosis,

CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural  
 CC scarring and glomerulonephritis, also (not claimed) osteoporosis),  
 CC or (ii) immune and inflammatory diseases (e.g. rheumatoid  
 CC arthritis, macrophage deficiency diseases or macrophage pathogen  
 CC infection). Nucleic acids encoding human antibody VH and VL can be  
 CC used for prodn. of recombinant antigen-binding domains. These are  
 CC highly specific, have low dissociation constants (pref. less than 5  
 CC nM) and low IC50s for neutralisation.  
 SQ Sequence 345 BP; 76 A; 112 G; 74 T;  
 Query Match 69.1%; Score 257; DB 33; Length 345;  
 Best Local Similarity 94.5%; Pred. No. 1.01e-158;  
 Matches 273; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 Db 1 gaggtgcagctggtggagctggtggagcgtgtccagcctggaggtccctgagactct 60  
 QY 1 GAGGTGCAGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 60  
 Db 61 tctgtgcagcgtctggagcttccagcttccagcttccagcttccagcttccagcttccagctt 120  
 QY 61 TCTGTGCAGGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 120  
 Db 121 ccagcgaagcgtggtggagctggtggagcgtgtccagcctggaggtccctgagactct 180  
 QY 121 CCAGGCAAGGCTGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 180  
 Db 181 gcagactccgtgaagcgttccagcttccagcttccagcgttccagcgttccagcgttccagc 240  
 QY 181 TCAGACTCCGTGAAAGGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 240  
 Db 241 ctgcaaatgagcagcctggagcgtggtggagcgttccagcgttccagcgttccagcgtt 289  
 QY 241 CTGCAAAATGAACAGCTGCACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 289  
 RESULT 3  
 ID Q78968 standard; DNA; 512 BP.  
 AC Q78968;  
 DT 03-AUG-1995 (first entry)  
 DE Human immunoglobulin Vh gene #30.  
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
 KW cosmid; placent; vector; pJB81; E.coli; mammalian; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 10..461  
 FT /product= human immunoglobulin variable heavy chain  
 FT /intron 56..156  
 FT /tag= b  
 FT /tag= c 462..464  
 FT /note= "miscellaneous signal, does not conform to  
 FT terminator or splice site sequence"  
 FT /terminator or splice site sequence"  
 PN W03425895-A.  
 PD 24-NOV-1994.  
 PF 10-MAY-1993; J006003.  
 PR 10-MAY-1993; WO-J006003.  
 PA (NTSB) JAPAN TOBACCO INC.  
 PI Honjo T., Matsuda F;  
 DR WPI: 95-006791/01.  
 DR P-PSDB: R66321.  
 PT DNA fragment comprising human immunoglobulin Vh genes - for the  
 PT production of human immunoglobulin in mammalian hosts  
 PS Claim 38; Page 69-70, 130pp, Japanese.  
 CC A series of genes (Q78968-79002) encoding human immunoglobulin variable  
 CC heavy chains. The genes were isolated and cloned from a series of cosmid  
 CC constructs: Y202; Y103; Y21; Y24; 3-31; M84; M18 and M131, by PCR  
 CC amplification using primers Q78917-38. The genes are subdivided into 5  
 CC families of Vh genes. The fragments cover a region of 800 kb. The DNA  
 CC fragments were isolated from high molecular weight DNA from human  
 CC placenta. The DNA was partially digested with TaqI restriction enzyme.  
 CC The fragments were separated by gel electrophoresis and 35-45 kb fractions  
 CC were collected. The fragments were ligated with ClaI digested cosmid

CC vector pJ81. The ligation products were in vitro packed and infected  
 CC into E.coli 490A. The fragments were then subcloned by colony  
 CC hybridisation. The Vh genes and the DNA fragments encoding them are  
 CC useful in producing human immunoglobulin in mammalian hosts  
 SQ Sequence 512 BP: 124 A: 104 G: 159 C: 125 T:

Query Match 69.1% Score 257; DB 13; Length 512;  
 Best Local Similarity 93.6%; Pred. No. 1.01e-158;  
 Matches 276; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 169 agtgcacactggtagagctggagggagcgtgggtccagccctggagcactct 228  
 Qy 2 AGTGCACACTGGTAGAGCTGGAGGGAGCGTGGTCCAGCCCTGGAGCACTCT 61  
 Db 229 cctctacacacctggagcttcacgttcacgttcacgttcacgttcacgttc 288  
 Qy 62 CCTCTACACACCTGGAGCTTCACGTTACGTTACGTTACGTTACGTTACGTT 121  
 Db 289 caggcagggggtggagtgagtgagtgagtgagtgagtgagtgagtgagtg 348  
 Qy 122 CAGGCAAGGGGTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181  
 Db 349 cagatccctggagggccacatccacatccacatccacatccacatccacat 408  
 Qy 192 CAGATCCCTGGAGGGCCACATCCACATCCACATCCACATCCACATCCACAT 241  
 Db 409 tccaaataaacacgtgagagctgaagacacggctgtgtattactatgcagaga 463  
 Qy 242 TCCAAATAAACACGTGAGAGCTGAAGACACGGCTGTGTATTACTATGCAGA 495

RESULT 4  
 ID T60380 standard: DNA: 369 BP.  
 AC T60380:  
 DT 27-NOV-1997 (first entry)  
 DE Anti-TGF beta-1 scfv antibody 1-82 Vh gene.  
 KW Transforming growth factor beta-1; TGF-beta-1; human;  
 KW antibody engineering; scfv; phage display; lung fibrosis;  
 KW arterial injury; proliferative retinopathy; retinal detachment;  
 KW adult respiratory distress syndrome; liver cirrhosis;  
 KW post myocardial infarction; post-angioplasty restenosis;  
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;  
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;  
 KW rheumatoid arthritis; macrophage deficiency disease;  
 KW macrophage pathogen infection; therapy; ss.  
 OS Homo sapiens  
 PN GR2305921-A.  
 PD 23-APR-1997.  
 PF 07-OCT-1996; 020920.  
 PR 14-JAN-1995; GB-001081.  
 PR 06-OCT-1995; GB-020486.  
 PA (CAMR-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Bacon L, Green JA, Jackson PH, Johnson KS, Pope AR:  
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ:  
 PI Wilton AJ:  
 DR WPI: 97-215360/20.  
 DR P-PSDB: W15534.  
 PT Agent contg. antigen-binding domain of human antibody to  
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding  
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,  
 PT immune and inflammatory disease  
 PS Example 1: Fig 1a(i); 184pp. English.  
 CC This DNA sequence comprises the gene encoding the Vh domain  
 CC (W1534) of human scfv antibody 1B2 (also known as 7A3), which  
 CC is specific for transforming growth factor (TGF) beta-1. It was  
 CC isolated by panning a phage antibody library produced from a  
 CC peripheral blood lymphocyte library. The antigen-binding domains  
 CC of human antibodies (see W1532-40) to TGF beta-1 and/or beta-2 can  
 CC be used to counter the adverse effects of TGF beta, such as (i)  
 CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung  
 CC fibrosis, arterial injury, proliferative retinopathy, retinal  
 CC detachment, adult respiratory distress syndrome, liver cirrhosis,  
 CC post myocardial infarction, post-angioplasty restenosis,

CC scleroderma, vascular disorders, cataract, glaucoma, or eff. renal  
 CC scarring and glomerulonephritis; also (not claimed) osteoporosis),  
 CC or (ii) immune and inflammatory diseases (e.g. rheumatoid  
 CC arthritis, macrophage deficiency diseases or macrophage pathogen  
 CC infection). Nucleic acids encoding human antibody Vh and VL can be  
 CC used for produ. of recombinant antigen-binding domains. These are  
 CC highly specific, have low dissociation constants (pref. less than 5  
 CC nM) and low IC50s for neutralisation.  
 SQ Sequence 469 BP: 87 A: 86 C: 115 G: 81 T:

Query Match 58.0% Score 253; DB 33; Length 369;  
 Best Local Similarity 93.5%; Pred. No. 6.82e-156;  
 Matches 272; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 2 aggtgcacactggtagagctggagggagcgtgggtccagccctggagcactct 61  
 Qy 2 AGTGCACACTGGTAGAGCTGGAGGGAGCGTGGTCCAGCCCTGGAGCACTCT 61  
 Db 62 cctctacacacctggagcttcacgttcacgttcacgttcacgttcacgttc 121  
 Qy 62 CCTCTACACACCTGGAGCTTCACGTTACGTTACGTTACGTTACGTTACGTT 121  
 Db 122 caggcagggggtggagtgagtgagtgagtgagtgagtgagtgagtgagtg 181  
 Qy 122 CAGGCAAGGGGTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181  
 Db 182 cagatccctggagggccacatccacatccacatccacatccacatccacat 241  
 Qy 182 CAGATCCCTGGAGGGCCACATCCACATCCACATCCACATCCACATCCACAT 241  
 Db 242 tccaaataaacacgtgagagctgaagacacggctgtgtattactatgcagaga 292  
 Qy 242 TCCAAATAAACACGTGAGAGCTGAAGACACGGCTGTGTATTACTATGCAGA 292

RESULT 5  
 ID T60381 standard: DNA: 369 BP.  
 AC T60381:  
 DT 27-NOV-1997 (first entry)  
 DE Anti-TGF beta-1 scfv antibody 31G9 Vh gene.  
 KW Transforming growth factor beta-1; TGF-beta-1; human;  
 KW antibody engineering; scfv; phage display; lung fibrosis;  
 KW arterial injury; proliferative retinopathy; retinal detachment;  
 KW adult respiratory distress syndrome; liver cirrhosis;  
 KW post myocardial infarction; post-angioplasty restenosis;  
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;  
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;  
 KW rheumatoid arthritis; macrophage deficiency disease;  
 KW macrophage pathogen infection; therapy; ss.  
 OS Homo sapiens.  
 PN GR2305921-A.  
 PD 23-APR-1997.  
 PF 07-OCT-1996; 020920.  
 PR 19-JAN-1995; GB-001081.  
 PR 06-OCT-1995; GB-020486.  
 PA (CAMR-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR:  
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ:  
 PI Wilton AJ:  
 DR WPI: 97-215360/20.  
 DR P-PSDB: W15535.  
 PT Agent contg. antigen-binding domain of human antibody to  
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding  
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,  
 PT immune and inflammatory disease  
 PS Example 1: Fig 1a(ii); 184pp. English.  
 CC This DNA sequence comprises the gene encoding the Vh domain  
 CC (W1535) of human scfv antibody 31G9, which is specific for  
 CC transforming growth factor (TGF) beta-1. It was isolated from  
 CC a large single chain fv library. The antigen-binding domains  
 CC of human antibodies (see W1532-40) to TGF beta-1 and/or beta-2 can  
 CC be used to counter the adverse effects of TGF beta, such as (i)  
 CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung

Key	Location/Qualifiers
sig_peptide	
/tag a	1..57
mat_peptide	
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US5648077-A.	
15-JUL-1997.	
05-SEP-1986.	904517.
21-APR-1992.	US-871426.
05-SEP-1986.	US-904517.
31-OCT-1986.	US-925196.
11-MAY-1988.	US-192754.
15-JUN-1990.	US-538796.
27-MAR-1991.	US-676036.
14-JUN-1994.	US-259372.
06-JUN-1995.	US-488671.
(SANO) SANDOZ LTD	
Oatberg LG.	
WPI; 97-372021/34.	
P-PSDB: W24984.	
Treatment of hepatitis B - with human monoclonal antibody	
Example 8; Column 15-18; 25pp; English.	
This is the nucleotide sequence encoding the heavy chain variable (VH) region from the human monoclonal antibody (MAB) PE1-1. The MAB was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating peripheral blood lymphocytes (PBL) and fusing them with a mouse/human xenogeneic cell line SP2-4. 5 cell lines were isolated.	









CC scarring and glomerulonephritis, also (not claimed) osteoporosis),  
 CC or (ii) immune and inflammatory diseases (e.g. rheumatoid  
 CC arthritis, macrophage deficiency diseases or macrophage pathogen  
 CC infection). Nucleic acids encoding human antibody VH and VL can be  
 CC used for prodn. of recombinant antigen-binding domains. These are  
 CC highly specific, have low dissociation constants (pref. less than 5  
 CC nM) and low IC50s for neutralisation.  
 SQ Sequence 369 BP; 85 A; 91 C; 115 G; 78 T;

Query Match 65.18; Score 242; DR 33; Length 369;  
 Best Local Similarity 91.78; Pred. No. 4.08e-148;  
 Matches 266; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Db 2 aggtgcaactggtgagctctggggagggcgctgctcagcctgggaggtccctggaactct 61  
 QY 2 AGGTGCACCTGCTGCACTCTGCGGAGCGGCTGCTCAGCCTGGAGGCTCCCTGACACTCT 61

Db 62 cctgtcagcctctgggactcaacttcagtagctatcaatgcaactgggtccgcagcctc 121  
 QY 62 CCTGTCCAGAGGCTGCGATTCACCTTCAGTCTTATGCGATGCACTGGGTCCGCGAGGCTC 121

Db 122 cagccaaagggtgagtggtggcgagttatcatcatatgagagtagtaataactatg 181  
 QY 122 CAGCCAAAGGCGTGGACTGGCTGCGGATATATGCTTCATGCAACTAATCAATCACTATT 181

Db 182 cagactccgtgaaggcggtgattcaccatctccagagacaaatcccaagaacacgctgtatc 241  
 QY 182 CAGACTCCGTGAAGGCGGATTCACGCTCTCCAGAGCAAAITCCAGAGACACGCGTGTTC 241

Db 242 tgcataatgaacagcctgagagctgagagacagcgctgtgtattactgtgcg 291  
 QY 242 TGCATAATGAACAGCCTGAGAGCCGAGGACACGCGCTGTCTATTACTGTGGG 291

RESULT 14  
 ID T60122 standard; cDNA; 357 BP.  
 AC T60122;  
 DT 15-MAY-1997 (first entry)  
 DE Coding sequence for heavy chain #4.  
 KW Antibody; heavy chain; light chain; variable region; human; monoclonal;  
 KW complementarity determining region; human; adr type hepatitis B virus;  
 KW HB virus; CDR: virus antigen; anti-HB antibody; vaccine; ss.  
 OS Homo sapiens.  
 PN J09020798-A.  
 PD 21-JAN-1997.  
 PE 11-JUL-1995; 174752.  
 PR 11-JUL-1995; JF-174752.  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 DR WPI: 97-140911/13.  
 DR P-PSDB; W13927.  
 PT Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine  
 PT vaccine  
 PS Claim 10; Page 17; 20pp; Japanese.  
 CC T60122-T60123 represent the coding sequences for the heavy and light  
 CC chains of the human monoclonal antibody of the invention. The antibody  
 CC of the invention preferably contains the sequence represented by W13912  
 CC in the complementarity determining region-1 (CDR-1) of the heavy chain  
 CC variable region. The antibody of the invention also contains the  
 CC sequence represented by W13913 in the CDR-3 of the light chain variable  
 CC region. The antibody is capable of binding to adr type hepatitis B (HB)  
 CC virus antigen. A human anti-HB virus monoclonal antibody preparation  
 CC which is highly safe and is effective to adr type HB virus can be  
 CC provided, using the monoclonal antibody. It can also be used as a  
 CC vaccine against HB infection.  
 SQ Sequence 357 BP, 76 A, 89 C, 115 G, 77 T,

Query Match 64.58; Score 240; DB 28; Length 357;  
 Best Local Similarity 91.78; Pred No 1.06e-146;  
 Matches 264; Conservative 0; Mismatches 24; Indels 0; Gaps 0.

Db 7 gctggtgagctggtggagagcgtggtccagcctggggggtccctggaactctctgtgc 66  
 QY 9 GCTGCTGAGCTGTGGGAGAGCGGTGCTGACCTGGGAGGTCCTGAGACTCTCTGTGCT 69

Db 67 agcgtctgattcaacttccagtagtgcagtgatgactggggggtccaggtccaggtcaa 125  
 QY 69 AGCGTTTGATTCACCTTCAGTGTATGTCATGTCATGTCATGTCATGTCATGTCATGTC 128

Db 127 ggggtggtgagtggtggcgacttatatgggtgcagcgactaataataattatgtgactc 186  
 QY 129 GGGGCTGGAGTGGGTGGCGAGGTATATGGTITGATGGAAGTAAATCAATCAATCAATCA 188

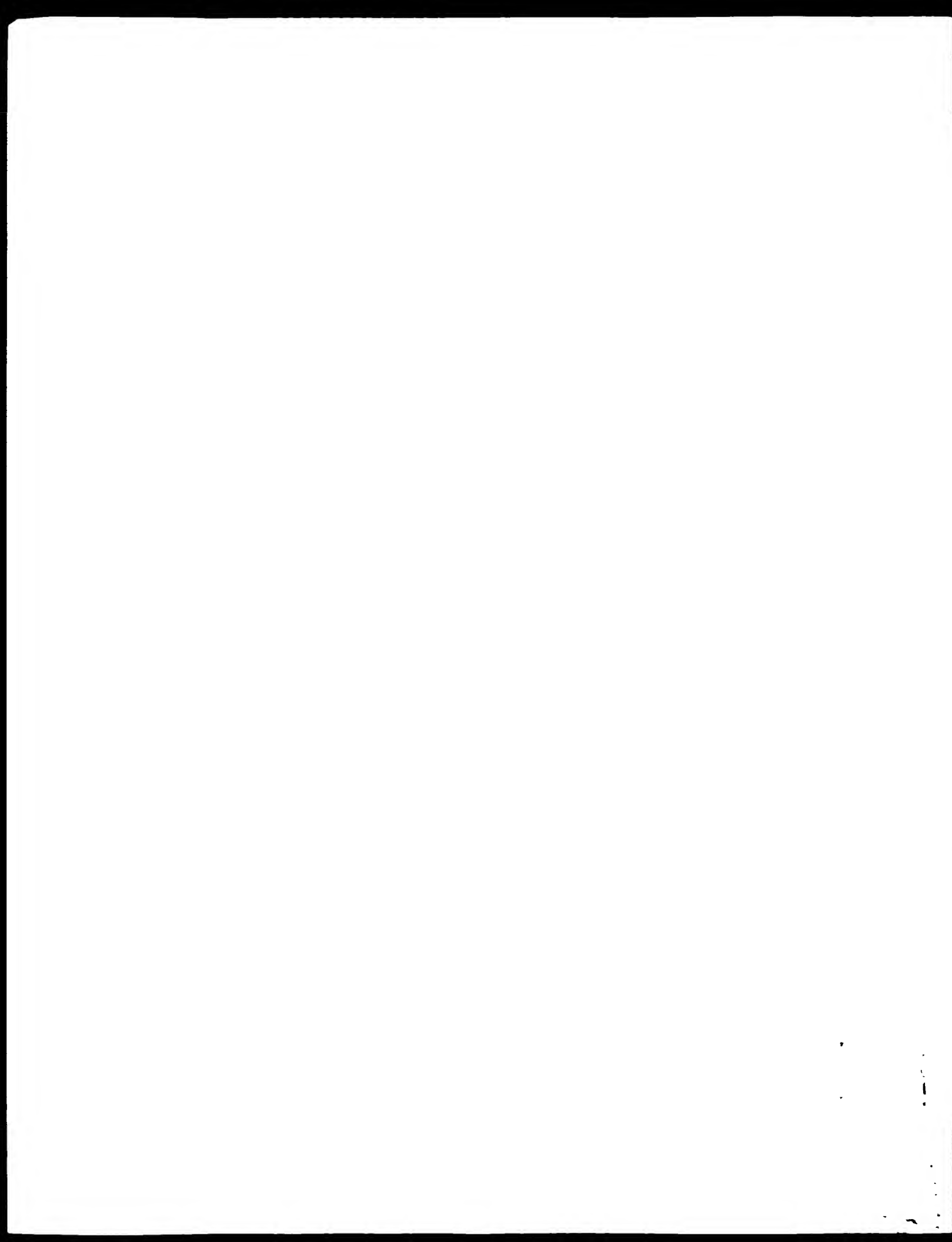
Db 187 cgtgaaagggccattccaccatctccagagcaaatccagaaacagctgactatctgagag 246  
 QY 189 CSTGAAGGGCCATTACCGCTTCCAGAGACAAITCCAGGAAACAGCGTGTITTTCTGCAAT 248

Db 247 gaacacccctgagagcgagggacagcgctgtgtattactgtgcgagaga 294  
 QY 249 GAACACCCCTGAGACCGGACGAGACACGCGCTGTCTATTACTGTCCGACAGA 296

RESULT 15  
 ID T60370 standard; DNA; 350 BP  
 AC T60370;  
 DT 27-NOV-1997 (first entry)  
 DE Anti-TGF beta-2 scFv antibody 2A-A9 VH gene.  
 KW Transforming growth factor beta-2; TGF-beta-2; human;  
 KW antibody engineering; scFv; phage display; lung fibrosis;  
 KW arterial injury; proliferative retinopathy; retinal detachment;  
 KW adult respiratory distress syndrome; liver cirrhosis;  
 KW post myocardial infarction; post-angioplasty restenosis;  
 KW scleroderma, vascular disease, cataract, glaucoma, scarring;  
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;  
 KW rheumatoid arthritis; macrophage deficiency disease;  
 KW macrophage pathogen infection; therapy; ss.  
 OS Chimeric Homo sapiens;  
 OS Chimeric synthetic.  
 PN GB2305921-A.  
 PD 23-APR-1997.  
 PE 07-OCT-1995; 020920.  
 PR 19-JAN-1995; GB-001081.  
 PR 06-OCT-1995; GB-020486.  
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;  
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;  
 PI Wilton AJ;  
 DR WPI: 97-215360/20.  
 DR P-PSDB; W15523.  
 PT Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and inflammatory disease  
 PT immune and inflammatory disease  
 PS Example 1; Fig 2a(ii); 184pp; English.  
 CC This DNA sequence comprises the gene encoding the VH domain (W15523) of human scFv antibody 2A-A9 (also known as 11E6), which is specific for transforming growth factor (TGF) beta-2. It was isolated by panning a phage antibody library produced from cloned germ-line V genes and synthetic CDPs. The antigen-binding domains of human antibodies (see W15523-40) to TGF beta 1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis) or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VI can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for neutralisation.  
 SQ Sequence 350 BP; 83 A; 87 C; 108 G; 72 T;

Query Match 64.08; Score 238; DB 33; Length 350;  
 Best Local Similarity 89.98; Pred. No. 2.73e-145;





and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
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2	268	72.0	523	95	523	HUM1GVB01M	Human IgH chain VDJC	2,540-223
3	267	71.8	366	95	366	HSV313148	H.sapiens rearranged	2,760-222
4	267	71.8	369	95	369	HSV30090	Human immunoglobulin	2,756-222
5	266	71.5	399	102	399	S64472	Immunoglobulin heavy	2,756-222
6	265	71.2	341	99	341	HUM1GCVABK	Human Ig germline Hc	2,376-220
7	265	71.2	342	93	342	HS1GCV01	H.sapiens mRNA for Hc	2,376-220
8	265	71.2	359	96	359	HSV31132	H.sapiens rearranged	2,376-220
9	265	71.2	366	99	366	HUM1GCVAA5	Human Ig germline Hc	2,376-220
10	265	71.2	375	91	375	HS1GCVB3	H.sapiens mRNA for Hc	2,376-220
11	265	71.2	375	95	375	HSJ03195	Human immunoglobulin	2,376-220
12	265	71.2	384	90	384	HSB10944	Human sapiens mRNA for	2,376-220
13	265	71.2	412	90	412	HUM1GCVAA1	Human sapiens germline	2,376-220
14	265	71.0	333	91	333	HS1GCV04	H.sapiens mRNA for Hc	2,306-219
15	264	71.0	363	95	363	HSJ03198	Human immunoglobulin	2,306-219
16	264	71.0	451	99	451	HUM1GHDJ0C	Human IgH chain VDJC	2,206-219
17	264	71.0	294	91	294	HS1GCVF0	H.sapiens germline Ig	2,246-218
18	263	70.7	294	91	294	HS1GCVH77	H.sapiens germline Ig	2,246-218
19	263	70.7	294	9	294	HS1GCVF0	H.sapiens germline Ig	2,246-218
20	263	70.7	365	91	365	HS1G04GVH	H.sapiens mRNA for Ig	2,246-218
21	263	70.7	377	95	377	HSJ03162	Human immunoglobulin	2,246-218
22	263	70.7	378	9	378	HSPE5AH	H.sapiens mRNA for Hc	2,246-218
23	263	70.7	378	93	378	HSPE6AH	H.sapiens mRNA for Hc	2,246-218
24	263	70.7	412	99	412	HUM1GCVAA1	Human germline IgH-chain	2,246-218
25	263	70.7	412	91	412	HS1GCVH28	H.sapiens germline Ig	2,246-218
26	263	70.7	529	95	529	HSJ031759	H.sapiens germline Ig	2,246-218
27	263	70.7	583	98	583	HUM1GCH333X	Human immunoglobulin	2,246-218
28	262	70.4	355	99	355	HUM1GCVHAA5	Human Ig germline Hc	1,906-217
29	262	70.4	355	99	355	HUM1GCVHAAU	Human Ig germline Hc	1,906-217
30	262	70.4	355	99	355	HUM1GCVHAA1	Human Ig germline Hc	1,906-217
31	262	70.4	355	99	355	HUM1GCVHAAW	Human Ig germline Hc	1,906-217
32	262	70.4	392	90	392	HSJ5535	H.sapiens rearranged	1,906-217
33	262	70.4	450	20	450	HSR0120	H.sapiens rearranged	1,906-217
34	262	70.4	696	96	696	HSJ02452	Human anti-HBsAg Igmu	1,906-217
35	261	70.2	341	93	341	HSJ033VAM	Human Ig germline Hc	1,746-216
36	261	70.2	341	99	341	HUM1GCVHAB1	Human Ig germline Hc	1,746-216
37	261	70.2	360	90	360	HUM1GCVHAA5	Human Ig germline Hc	1,746-216
38	261	70.2	363	95	363	HSJ06107	Human immunoglobulin	1,746-216
39	261	70.2	420	90	420	HSJ0513	H.sapiens rearranged	1,636-215
40	260	69.9	363	95	363	HUM1GCVHAA5	Human Ig germline Hc	1,636-214
41	259	69.6	363	95	363	HSJ06161	Human immunoglobulin	1,636-214
42	259	69.6	373	101	373	HS1GCVH37	Human mRNA for Igmu	1,636-214
43	259	69.6	375	95	375	HSJ06103	Human immunoglobulin	1,636-214
44	259	69.6	366	91	366	HS1GCVH07	H.sapiens rearranged	1,636-214
45	259	69.6	366	91	366	HS1GCVH07	H.sapiens rearranged	1,636-214

## ALIGNMENTS

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	ACCESSION		L23571				
	NID		3388021				
	KEYWORDS		J-region; J-region; immunoglobulin; heavy chain.				
	SOURCE		Homo sapiens adult peripheral blood cDNA to mRNA.				
	ORGANISM		Homo sapiens				
			Eukaryotae; Eukaryotae; Metazoa; Chordata;				
			Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo;				
	REFERENCE		1. (bases 1 to 454)				
	AUTHORS		Chai, S.K., Kasaian, M.J., Ikematsu, H., Kim, M.Y. and Casali, P.				
	TITLE		VH-DJH gene sequences of mAb produced by human P-10, P-1b, and B-2 cells				
	JOURNAL		Unpublished (1993)				
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BASE COUNT  
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Matches 327; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db 173 caggcaagggtggtggtgggtggtggtatggtatggtatggtatggtatggtatggtatg 232
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCAGGTATATGTTTGTATGTAATTAATCAATACTATT 181
Db 233 cagactccatgaaggccgattcacctatctccagagacaattcccaagacacgctgtatc 292
QY 182 CACACTCCCTGACAGCGCGGATATCACCGCTCTCCAGAGACAATTCACGAGACACCGCTGTTT 241
Db 293 tgcaaatgaacacgctgagagccgagagacacgctgtgtattactgtgcgagaccagtat 352
QY 242 TGCAAATGAACACGCTGAGAGCCGAGACACACGCGTGTCTATTACTGTCCGACAGAGTAC 301
Db 353 tactatggttcaggagccctcaactcagctgttcagccctgggcccaggaaccctaatca 412
QY 302 TTTTGTGATGCATTAAAGGGGCGTACTACCTTGAANAATGSGGSCACAGGSAACCTGTGACA 361
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QY 362 CCCTCTCTCTCA 372

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RESULT 2 HMTSHQJCM 523 bp mpna PPI 09-NOV-1994  
LOCUS Human Igh chain VDJ<sub>H</sub> region mpna, partial cds  
DEFINITION Human Igh chain VDJ<sub>H</sub> region mpna, partial cds  
ACCESSION L23567  
NID 9499609

KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;  
SOURCE Homo sapiens (individual isolate Donor R) adult peripheral blood  
CDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS Chal, S.K., Kasalan, M.T., Ikematsu, H., Kim, M.Y. and Casali, P.  
TITLE VH-D-JH gene sequences of mAb produced by human B-1a, B-1b, and B-2  
cells  
JOURNAL Unpublished (1994)  
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gene

V\_segment

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D\_segment

J\_segment

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Matches 327; Conservative 0; Mismatches 41; Indels 3; Gaps 3;

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QY 2 AGGTGTCAGCTGCTGAGTCTGGGGAGAGGCTGTGTCAGCTGGAGGTCCTGAGACTCT 61  
Db 113 cctgtgcagctgtgattcaccttcagctagctatggtcagctgggtccgcccaggctc 172



LEWAVAVISYDGSNXYADSVKGRFTTSPDNKNTLYLQMNLSLPAEDTAVVYCARGLLL

BASE COUNT 80 a 89 c 113 g 86 t  
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Query Match 71.8%; Score 267; DR 95; Length 368;  
 Best Local Similarity 88.7%; Pred. No. 2,750-222;  
 Matches 329; Conservative 0; Mismatches 38; Indels 4; Gaps 4;

Db 2 aggtgcagctggtggagctctggggagagcgtgggtccagcctgggggtccctgagactct 61  
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Db 62 cctgtgcagcctctggatccactccatagctatgcatgcatgcatgcatgcatgcatg 121  
 QY 62 CTTGTGCAGCGTCTGGATTCACCTTCAGTCTTATGGCATGCACTGGGTGCGCCAGGCTC 121

Db 122 cagcgaagggtgagtggtggcaggttatcatatgatgatggaagtaataataactatg 181  
 QY 122 CAGCGAAGGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181

Db 182 cagactccctgagggccgattccaccatctccagagacattccaaagacacgcgtgtatc 241  
 QY 182 CAGACTCCCTGAGGGCCGATTCCACCATCTCCAGAGACAAATCCAGGAAACACGCTGTTC 241

Db 242 tgcgaatgagcagcctgagagctgagagcagcgtgtgtattactgtgcgagagccctt- 300  
 QY 242 TGCGAATGAGCAGCCTGAGAGCTGAGAGCAGGACAGCGGTGTATTACTGTGCGACAGAGGTAC 301

Db 301 ttattgtagtggtgagct-gct-c-actttgactactggggcagggaaacccctgtgca 357  
 QY 301 TTTTGGATCGATTAGGGGCGTTACTACTTGTAAACCTGGGGCAGGAAACCCCTGTGCA 361

Db 358 cccctctctctca 368  
 QY 362 CCGTCTCTCTCA 372

RESULT 5 S64471 399 bp mRNA PRI 10-JUL-1992  
 LOCUS Immunoglobulin heavy chain V region [human, X-linked  
 DEFINITION agammaglobulinemia patients, B lymphoblastoid cell lines, mRNA  
 Partial, 399 nt].  
 ACCESSION S64471  
 NID g236904  
 KEYWORDS human B lymphoblastoid cell lines X-linked agammaglobulinemia  
 SOURCE patients.  
 ORGANISM Homo sapiens  
 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo  
 Timmers, E., Kenter, M., Thompson, A., Kraakman, M. E., Bertram, T. E.,  
 Alt, F. W., and Schuurman, P. K.  
 AUTHORS Diversity of immunoglobulin heavy chain gene segment rearrangement  
 TITLE in B lymphoblastoid cell lines from X-linked agammaglobulinemia  
 patients  
 JOURNAL Eur J. Immunol 21 (12): 2355-2363 (1991)  
 MEDLINE 92098140  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 54471] from the original journal article.  
 This sequence comes from Fig.1a.  
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 /translation="VULVESGGGVVLPSPSLKLSAASGLIFSSYEMHWLQAPKGL  
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 BASE COUNT 89 a 106 c 120 g 84 t  
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Query Match 71.5%; Score 266; DR 102; Length 369;  
 Best Local Similarity 87.9%; Pred. No. 2,560-221;  
 Matches 326; Conservative 0; Mismatches 42; Indels 3; Gaps 3;

Db 2 aggtgcagctggtggagctctggggagagcgtgggtccagcctgggggtccctgagactct 61  
 QY 2 AGGTGCAGCTGCTCGAGTCTGGGGAGAGCGTGTCCAGCCTGGAGAGTCTCTGAGACTCT 61

Db 62 cctgtgcagcctctggatccactccatagctatgcatgcatgcatgcatgcatgcatg 121  
 QY 62 CTTGTGCAGCGTCTGGATTCACCTTCAGTCTTATGGCATGCACTGGGTGCGCCAGGCTC 121

Db 122 cagcgaagggtgagtggtggcaggttatcatatgatgatggaagtaataataactatg 181  
 QY 122 CAGCGAAGGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181

Db 182 cagactccctgagggccgattccaccatctccagagacattccaaagacacgcgtgtatc 241  
 QY 182 CAGACTCCCTGAGGGCCGATTCCACCATCTCCAGAGACAAATCCAGGAAACACGCTGTTC 241

Db 242 tgcgaatgagcagcctgagagctgagagcagcgtgtgtattactgtgcgagagccctgca 301  
 QY 242 TGCGAATGAGCAGCCTGAGAGCTGAGAGCAGGACAGCGGTGTATTACTGTGCGACAGAGGTAC 301

Db 302 gactcag-tatagca-gcagc-tggggaatttgactactggggcagggaaacccctgtgca 358  
 QY 302 TTTTGGATCGATTAGGGGCGTTACTACTTGTAAACCTGGGGCAGGAAACCCCTGTGCA 361

Db 359 cccctctctca 369  
 QY 362 CCGTCTCTCTCA 372

RESULT 6 HUMIGHYABK 341 bp DNA PRI 03-JAN-1995  
 LOCUS Human Ig germline H-chain gene V-region, clones b0-12.33.35.  
 DEFINITION  
 ACCESSION M77333  
 NID g185761  
 KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain.  
 SOURCE Homo sapiens (individual isolate b0j) adult DNA.  
 ORGANISM Homo sapiens  
 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 Glee, T., Yang, P. M., Stiminovitch, K. A., Olsen, N. T., Hillson, J.,  
 Wu, J., Kozic, F., Carson, D. A., and Chen, P. P.  
 AUTHORS Molecular basis of an autoantibody-associated restriction fragment  
 length polymorphism that confers susceptibility to autoimmune  
 diseases  
 JOURNAL J. Clin Invest 88 (1): 193-203 (1991)  
 MEDLINE 91277280  
 REMARK Location/Qualifiers  
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/note="7 mer recombination signal"
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Best Local Similarity 94.9%   Prod No. 2.37e-220;
Matches 280;   Conservative 0;   Mismatches 15;   Indels 0;   Gaps 0;

Db 42 agtgcagctggtgagctctgagagagcgtgagagagcgtgagagagcgtgagagctct 101
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QY 2 AGGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
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Db 102 cctgtgcagctctgagagcgtctgagagagcgtctgagagagcgtctgagagagcgtc 161
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QY 62 CGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
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Db 162 cagagcagagggctgagagagcgtctgagagagcgtctgagagagcgtctgagagagcgt 221
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QY 122 CAGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
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Db 222 cagagcagagggctgagagagcgtctgagagagcgtctgagagagcgtctgagagagcgt 281
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QY 182 CAGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
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Db 282 tgcagcagagggctgagagagcgtctgagagagcgtctgagagagcgtctgagagagcgt 336
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QY 242 TGCAGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 296
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RESULT 7
LOCUS      HSHVCVDL1      342 bp      RNA      PFI      20-JAN-1997
DEFINITION H.sapiens mRNA for rearranged Ig heavy chain variable domain,
            cell-type RA-1-DT7.
ACCESSION  X99362
NID        q1480264
KEYWORDS   immunoglobulin: variable region.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 342)
AUTHORS    Djavad N., Bas, S., Shi, X., Schwager, J., Jeannot, M., Vischer, T. and
            Roosnek, E.
TITLE      Comparison of rheumatoid factors of rheumatoid arthritis patients,
            of individuals with mycobacterial infections and of normal
            controls: evidence for maturation in the absence of an autoimmune
            response
JOURNAL    Eur. J. Immunol. 25 (10), 2480-2486 (1996)
MEDLINE    97054666
REFERENCE  2 (bases 1 to 342)
AUTHORS    Proosnek, E.
TITLE      Direct Submission
JOURNAL    Submitted (05-JUL-1996) E. Proosnek, HCG, Unite d immunologie de
            transplacation, 24, Rue Micheli-du-Crest 1211 Geneva 14,
            Switzerland
FEATURES   Location/Qualifiers
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SYVYSGSIFDP"
BASE COUNT      79 a   76 c   104 g   83 t
ORIGIN
Query Match      71.2%   Score 265;   DB 91;   Length 312;
Best Local Similarity 94.9%   Prod No. 2.37e-220;
Matches 280;   Conservative 0;   Mismatches 15;   Indels 0;   Gaps 0;

Db 2 aggtgcagctggtgagcgtctgagagagcgtctgagagagcgtctgagagagcgtctgag 61
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QY 2 AGGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
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Db 62 cctgtgcagcctctgagcgtctgagagagcgtctgagagagcgtctgagagagcgtctgag 121
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QY 62 CGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
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Db 122 cagagcagagggctgagagagcgtctgagagagcgtctgagagagcgtctgagagagcgt 181
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QY 122 CAGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
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QY 182 CAGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
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QY 242 TGCAGTGTGACAGCTGCTGTAATCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 296
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RESULT 8
LOCUS      HSHVC132      309 bp      RNA      PFI      12-JUN-1992
DEFINITION H.sapiens rearranged mRNA for fetal Ig heavy chain VH3, DQ52, a
            possible inverted Dm2 (overlapping with DQ52), and Jh3 (clone
            FL13-2).
ACCESSION  X62959
NID        g37675
KEYWORDS   Ig CDR3 region; Ig heavy chain; Jh element; rearranged gene; Vh
            element.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 359)
AUTHORS    Paaphorst, F. M., Timmers, E., Koster, M. J., Van Tol, M. J., Vessels, J. M.,
            and Schuurman, R. K.
TITLE      Restricted utilization of germ-line Vh3 genes and short diverse
            third complementarity-determining regions (CDR3) in human fetal B
            lymphocyte immunoglobulin heavy chain rearrangements
JOURNAL    Eur. J. Immunol. 22 (1), 247-251 (1992)
MEDLINE    92111633
REFERENCE  2 (bases 1 to 359)
AUTHORS    Paaphorst, F. M.
TITLE      Direct Submission
JOURNAL    Submitted (31-oct-1991) F. M. Paaphorst, Division of Immunology,
            Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden,
            Building 17, E3-Q, P.O.Box 9600, 2300 Leiden, THE NETHERLANDS
COMMENT    For related sequences see X62954-X62972, X62612-3, X62677,
            Schroeder H W Jr, et al, Proc Natl Acad Sci USA, 87:6149 (1990) &
            Ichihara Y, et al, Eur. J. Immunol. 18:649 (1988).
FEATURES   Location/Qualifiers
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Best Local Similarity 94.9%; Pred No 2 37e-220;
Matches 280; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db 62 cctgtgcagctgtgagctgtcccttcagtagctatgcatgcatgcatgcatgcatgcatgcat 121
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Qy 122 CAGGCAAGGCGTGAAGGCGCGATTCACCGTCTCCAGAGCAATTCAGGACACGCGTCTTC 241
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Db 182 cagactcgtggaagggccgattccattccagtagctatgcatgcatgcatgcatgcatgcatgcat 241
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Db 242 tcaataaacagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 295
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RESULT 9 HUMIGHYAAS 360 bp DNA PRI 03-JAN-1995
LOCUS Human Ig germline H-chain gene V-region, clone Nov.
DEFINITION M77315
ACCESSION 9185725
NID
KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 360)
AUTHORS Olee,T., Yang,P.M., Siminovich,K.A., Olsen,N.J., Hillson,J., Wu,J., Korin,F., Carson,D.A. and Chen,P.P.
TITLE Molecular basis of an autoantibody-associated restriction fragment length polymorphism that confers susceptibility to autoimmune diseases
JOURNAL J Clin. Invest. 88 (1), 193-203 (1991)
MEDLINE 91277280
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/note="7 mer recombination signal"
BASE COUNT 80 a 80 c 116 g 84 t
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Best Local Similarity 94.9%; Pred. No. 2.37e-220;
Matches 280; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 42 aggtgcagctgtgagctgtggggagggcgtgggtccagcctggggaggtccctgaaactct 101
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Qy 2 AGGTGCAGCTGTGAGCTGTGGGGAGGGCGTGGGTCCAGCCTGGGGAGGTCCCTGAAACTCT 101
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Db 102 cctgtgcagctgtgagctgtcccttcagtagctatgcatgcatgcatgcatgcatgcatgcat 161
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Qy 62 CCTGTGCAGCTGTGAGCTGTCCCTTCAGTAGCTATGCTATGCTATGCTATGCTATGCTATGCT 121
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Db 162 caggcaagggtgagtggtgagcagttatgtgtatgtatgtatgtatgtatgtatgtatgt 221
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Qy 122 CAGGCAAGGCGTGAAGGCGGATTCACCGTCTCCAGAGCAATTCAGGACACGCGTCTTC 241
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Db 222 cagactcgtggaagggccgattccattccagtagctatgcatgcatgcatgcatgcatgcatgcat 281
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Qy 182 CAGACTCGTGGAAGGGCGGATTCACCGTCTCCAGAGCAATTCAGGACACGCGTCTTC 241
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Db 282 tgcataaacagcagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 336
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Qy 242 TGCATAAACAGCAGCCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 296
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RESULT 10 HSHAMBH 375 bp RNA PRI 10-MAR-1993
LOCUS H sapiens mRNA for HamRH heavy chain variable Ig domain.
DEFINITION X64154
ACCESSION 938353
NID
KEYWORDS heavy chain; Ig heavy chain; immunoglobulin heavy chain variable region; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 375)
AUTHORS Hughes-Jones,N.C.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992) N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research, Babraham Hall, Cambridge CB2 4AT, UK
REFERENCE 2 (bases 1 to 375)
AUTHORS Bye,J.M., Carter,C., Cui,Y., Gorick,P.D., Songsivilai,S., Winter,G., Hughes-Jones,N.C. and Marks,J.D.
TITLE Germine variable region gene segment derivation of human monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation by somatic hypermutation and repertoire shift
J Clin Invest. 90 (6), 2491-2496 (1992)
MEDLINE 93107334
COMMENT See also X64148-69.
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REFERENCE   1 (bases 1 to 375)
AUTHORS     Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE       Analysis of rearranged immunoglobulin heavy chain variable region
            genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL     Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE     97182739
REFERENCE   2 (bases 1 to 375)
AUTHORS     Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE       Direct Submission
JOURNAL     Submitted (26-Nov-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
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            RAIAAANWDPWGQGLTVVSS"
BASE COUNT      89 a 97 c 113 g 76 t
ORIGIN
Query Match. 71.2%, Score 265, DB 95, Length 375;
Best Local Similarity 87.4%; Pred. No. 2,370-220;
Matches 327; Conservative 0; Mismatches 44; Indels 3; Gaps 2;
Db 2 aggtgcagctgtgagctctggggaggagcgtggtccagcctggaggtccctgagactct 61
QY 2 AGGTGCAGCTGTGCTGAGCTGTGGGGAGGAGCGTGGTCCAGCCTGGAGGTCCTGAGACTCT 61
Db 62 cctgtgcagcctctgattccacttcagtagctatggcctacactgggtccgcaggctc 121
QY 62 CCTGTGCAGCCTCTGATTCCACTTCAGTGTATGGCATACACTGGGTCCGCAGGCTC 121
Db 122 caggcaagggtctgagtggtggcagttatcatatgatggaagtaataaactatg 181
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Db 182 cagatctcctgaaggcagctatccactcctcagaagacaa+tcacagaacacgctgctc 241
QY 182 CAGACTCTCTGAAGGCGGCGATTACCTGCTCTCAGAGACAATTCAGGAACACGCTGTTTC 241
Db 242 tgcacatgacacagctggagctggaggacacaggtgtgtatattactgtgagagatccga 301
QY 242 TGCACATGAACAGCTGAGACCGGAGGAGACCGGCTGTCTATTACTGTGCCAGAGAGGTAC 301
Db 302 ataaagagcgtatancagcagcccccaactaggttcgacccctggggccagggaacctgg 361
QY 302 TTTTTCGATCGATTAAAGGGGGGTTT--ACTACTTGAAATATGGGGCCAGGGACCCCTGC 368
Db 362 tcaccgtctctctca 375
QY 369 TCACCGCTCTCTCA 372

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RESULT      13
LOCUS       HSRUP94H      384 bp      RNA      PRI      28-OCT-1994
DEFINITION Homo sapiens mRNA for anti-Sm antibody VH chain (VH3/JH6).
ACCESSION   Z46379
KEYWORDS    5587147
            anti-Sm antibody; diversity region; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 384)
AUTHORS     Mahmoudi,M., Edwards,J., Cairns,E. and Reil,P.
TITLE       Molecular characterization of natural human anti-Sm autoantibodies
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 384)
AUTHORS     Mahmoudi,M.
TITLE       Direct Submission
JOURNAL     Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario,
            Medicine and Microbiology and Immunology, University Hospital Room
            B8E-12, London, Ontario, Canada, N6A 5A5
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            /clone="BUD94"
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            /cell_type="B-cell"
            1..>384
            /note="Author-given protein sequence is in conflict with
            the conceptual translation."
            /codon_start=1
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            /translation="QVQLVESGGGVQPGSLRFLSCAASGFTFSYGMHWVQAPGKG
            LEWAVIVYDGSNKKYADSVKGRFTISPDNSKNTLYLQNSLPAEDTAVVYCARDNVY
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gene        1..294
            /gene="hv3019b9"
V_segment   1..294
            /gene="hv3019b9"
            /note="VH segment"
D_segment   295..324
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gene        295..324
            /gene="DXP4"
J_segment   325..384
            /note="JH6 region"
BASE COUNT      91 a 88 c 116 g 89 t
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Best Local Similarity 94.9%; Pred. No. 2,370-220;
Matches 280; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Db 2 aggtgcagctgtgagctctggggaggagcgtggtccagcctggaggtccctgagactct 61
QY 2 AGGTGCAGCTGTGCTGAGCTGTGGGGAGGAGCGTGGTCCAGCCTGGAGGTCCTGAGACTCT 61
Db 62 cctgtgcagcctctgattccacttcagtagctatggcctacactgggtccgcaggctc 121
QY 62 CCTGTGCAGCCTCTGATTCCACTTCAGTGTATGGCATACACTGGGTCCGCAGGCTC 121
Db 122 cagcaaaagggtctgagctgggtggcagttatcatatgatggaagtaataaactatg 181
QY 122 CAGCAAAAGGCTCTGAGTGGTGGCAGGTATATGTTTATGGAAGTAATCAATACTATT 181
Db 182 cagatctcctgaaggcagctatccactcctcagaagacaa+tcacagaacacgctgctc 241
QY 182 CAGACTCTCTGAAGGCGGCGATTACCTGCTCTCAGAGACAATTCAGGAACACGCTGTTTC 241
Db 242 tgcacatgacacagctggagctggaggacacaggtgtgtatattactgtgagagatccga 296
QY 242 TGCACATGAACAGCTGAGACCGGAGGAGACCGGCTGTCTATTACTGTGCCAGAGAGGTAC 296

```



1











Washington University School of Medicine  
4444 Forest Park Parkway, Box 800, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1910

Email: [estwatson.wustl.edu](mailto:estwatson.wustl.edu)  
This clone is available royalty-free through INL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information  
Seq primer: -28ml3 rev2 F1 from AmerSham  
High quality sequence stop: 161.

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
/notes="Gran. Ovary: Vector: pT73D (Phar
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strand cDNA was primed with a Not I - c
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double-stranded cDNA was size selected,
adapters (Pharmacia), digested with Not
the Not I and Eco RI sites of a modified
(Pharmacia). Library constructed by Bent
M.Fatima Bonaldo."
/clone="810346"
/clone.lib="Scars ovary tumor NbOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10 (ampicillin resistant)"
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/db_xref="GBR:6040648" 72
69 a 102 c 82 c
MPNA
BASE COUNT

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Query Muscl. 49.5%, Score 156, Du 16, Length 324,  
Best Local Similarity 95.24, Freq. No. 1,520+28;  
Matches 206; Conservative 0; Mismatches 20; Indels 5; Gaps 5.

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Qy       7  AGCGATCTTCAGTACGTTACTGTCTGTCTCTCAGGGAAAAAGGCTTCCCTGTATGTCAGG 66  
  
Dbb     140  ggcattcgagadtttatcaccaacttatacttgatccagcagcatctctggccagctccc 199  
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy      57  GCACATCATATCTTGTAACAAATTATATCTTATATCAACAATAAACCTTGGTCAAGCTCCC 156  
  
Dbb     200  aggtctctctctctctggtatctacacacagagacacacttatctccacagcaggtctgaagatg 259  
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy     127  AGGCCTCTCATTTATGTAAGAACCACAGACAGGCACTGATATCTTCACAGAGTITTAGTGG 185  
  
Dbb     260  catggaatcagggacagagattctactcttcacacattccagcagcagctcaggt 310  
  
Qy     186  CATGTCCTCTCTGGACAGAGATTCAGAGCTCTCATCATTCAGCAAGCTTGGTCAAGT 232
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RESULT	8
LOCUS	AA485616
DEFINITION	240 bp mRNA EST 24-JUN-1997
DESCRIPTION	zx3ohol t1 Soares ovary tumor NH01 homo sapiens CDNA clone #11057 5' similar to gb-M12740_cds1 IG KAPPA CHAIN PRECURSOR V-HI REGION (HUMAN);..
ACCESSION	AA485616
NID	Q2214835
KEYWORDS	EST..
SOURCE	human
ORGANISM	homo sapiens
	Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata:
	Eukaryotae: Vertebrata: Eutheria: Primates: Catarrhini: Hominidae:

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1. (bases 1 to 240)  
Hillier, B., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Krabat, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
Theising, B., White, Y., Wylie, I., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)

Contact: Wilson PK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63104  
Tel: 314 246 1800  
Tel: 314 246 1800  
Fax: 314 286 1810  
Email: estewartson.wustl.edu  
This clone is available royalty-free through LBNL. Contact the  
IMAGE Consortium ([image.lbl.gov](http://image.lbl.gov)) for further information.  
Seq primer: -28m13 rev2 EI from Amersham.

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FEATURES
source
Location/qualifiers
11.240

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1.240
/organism="Homo sapiens"
/notes="Organ: Ovary; Vector: pT73D (Pharmacia) modified polylinker, Site 1: Not I, Site 2: EcoRI; cDNA: 1.2 kb; cDNA strand cDNA was primed with a Not I - EcoRI linker. The cDNA was amplified with the primers: 5'-TGAATTCATCTCAATGCGACGCGCGGTTTITTTT-3' and 5'-TGAATTCATCTCAATGCGACGCGCGGTTTITTTT-3'. The cDNA was then digested with Not I and EcoRI. The cDNA was then ligated into the Not I and EcoRI sites of a modified (Pharmacia). Library constructed by Bent M. Ratina Bonaldo."
/clone="11057"
/clone_gib="Scars Ovary tumor NbHOT"
/sex="Female"
/tissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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</db_xref="GDB:604166"
54 a 80 c 59 g 47 t

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[illegible]

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IL	HS120478	
AC	AA485616;	
NI	G214835	
DI	27-JUN-1997 (Pol. 52, Created)	
DI	27-JUN-1997 (Pol. 52, Last updated, Version 1)	
DF	790901.1 Scores ovary tumor Nshot Homo sapiens cDNA clone 811057	
DF	5' similar to gb:M12740.cd1.13 KAPPA CHAIN PEPUSAP V-11 REGION	
DE	(HUMAN) ;	
DE	EST.	
KW	EST.	
OS	Homo sapiens (human)	
OC	Eukaryotes	
OC	Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:	
OC	Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae:	
OC	Homo	

[1]  
 1-240  
 RP Hillier I, Allen M, Powles I, Dubouque T, Geisel G., Gust S.,  
 PA Krimman D., Kucaba T., Lacy M., Le N., Lesoski G., Maria M.,  
 PA Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,  
 PA Theising B., Whitely Y., Wyllie T., Waterston R., Wilson R.,  
 RT "WashU-NCI human EST Project";  
 FL unpublished.  
 FL Contact: Wilson PK Washington University School of Medicine 4444  
 FCC Forest Park Parkway, Box 4501, St. Louis, MO 63118 Tel: 314 286  
 CCC 1800 Fax: 314 296 1810 E-mail: wustl@wustl.edu This clone is





Query Match 40.0%; Score 126; DB 29; Length 242;  
 Best Local Similarity 91.4%; Pred. No. 4.04e-197;  
 Matches 139; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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 Db 151 gaggtagcagcaacttagctggtagcaggggaagagccaccctctctctgagggccaggtct 210  
 QY 75 GAGGTGCGGTAAACAATTTAGCTTGGTATCAGCAGAAACCTGCGCAGGCTCCAGGCTCT 134  
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 QY 135 CATTATTGTTGGAAACACCAAGCCACTGGTA 166

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 DT 24-JUN-1997 (Rel. 52, Created)  
 DT 24-JUN-1997 (Rel. 52, Last updated, Version 1)  
 DE zv29d06.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 755051  
 DE 5' similar to gb:M12740\_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION  
 DE (HUMAN);.  
 KW EST.  
 OS Homo sapiens (human)  
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP 1-242  
 PA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,  
 RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,  
 RA Moore R., Schellenberg K., Steptoe M., Tan F., Theising R.,  
 RA White Y., Wylie T., Waterston R., Wilson R.;  
 RT "WashU-NCI human EST Project";  
 RL Unpublished.  
 CC Contact: Wilson RK Washington University School of Medicine 4444  
 CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286  
 CC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is  
 CC available royalty-free through LNL; contact the IMAGE Consortium  
 CC (info@image.lnl.gov) for further information. Seq primer: -28m13  
 CC rev2 ET from Amersham.  
 FH Key Location/Qualifiers  
 FH source 1..242  
 FT /organism="Homo sapiens"  
 FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a  
 FT modified polylinker; Site\_1: Not 1, Site\_2: Eco RI, 1st  
 FT strand cDNA was primed with a Not I - oligo(dT) primer (5'  
 FT TGTACCAATCTGAAGTGGCAGCGCGCGGTCTTTTCTTTTCTTTT 3').  
 FT TGTACCAATCTGAAGTGGCAGCGCGCGGTCTTTTCTTTTCTTTT 3').  
 FT double-stranded cDNA was size selected, ligated to Eco RI  
 FT adapters (Pharmacia), digested with Not I and cloned into  
 FT the Not I and Eco RI sites of a modified pT73 vector  
 FT (Pharmacia). Library constructed by Bento Soares and  
 FT M.Fatima Bonaldo."  
 FT /clone="755051"  
 FT /clone\_lib="Soares ovary tumor NBHOT"  
 FT /sex="Female"  
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 FT mRNA  
 SQ Sequence 242 RF 54 A, 82 C, 59 G, 47 T, 0 other;

Query Match 40.0%; Score 126; DB 65; Length 242;  
 Best Local Similarity 91.4%; Pred. No. 4.04e-197;  
 Matches 139; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 91 tccagccaccctgtctgtctccaggggaagagccaccctctctctgagggccaggtca 150  
 QY 15 TCCAGCCACCCTGTCTGTCTCCAGGGGAAGAGCCACCCTCTCTCTGAGGGCCAGTCA 74

Db 151 gaggtagcagcaacttagctggtagcaggggaagagccaccctctctctgagggccaggtct 210  
 QY 75 GAGGTGCGGTAAACAATTTAGCTTGGTATCAGCAGAAACCTGCGCAGGCTCCAGGCTCT 134  
 Db 211 catctatggtgcacatccaccaggccactggtta 242  
 QY 135 CATTATTGTTGGAAACACCAAGCCACTGGTA 166

RESULT 15  
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 AC AA464647;  
 NI 92189531  
 DT 13-JUN-1997 (Rel. 52, Created)  
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 DE zx85b12.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 810527  
 DE 5' similar to gb:M12740\_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION  
 DE (HUMAN);.  
 KW EST.  
 OS Homo sapiens (human)  
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
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 RA Moore R., Schellenberg K., Steptoe M., Tan F., Theising R.,  
 RA White Y., Wylie T., Waterston R., Wilson R.;  
 RT "WashU-Merck EST Project 1997";  
 RL Unpublished.  
 CC Contact: Wilson RK WashU-Merck EST Project Washington University  
 CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
 CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through  
 CC LNL; contact the IMAGE Consortium (info@image.lnl.gov) for  
 CC further information. Seq primer: -28m13 rev2 ET from Amersham.  
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 FT strand cDNA was primed with a Not I - oligo(dT) primer (5'  
 FT TGTACCAATCTGAAGTGGCAGCGCGCGGTCTTTTCTTTTCTTTT 3').  
 FT TGTACCAATCTGAAGTGGCAGCGCGCGGTCTTTTCTTTTCTTTT 3').  
 FT double-stranded cDNA was size selected, ligated to Eco RI  
 FT adapters (Pharmacia), digested with Not I and cloned into  
 FT the Not I and Eco RI sites of a modified pT73 vector  
 FT (Pharmacia). Library constructed by Bento Soares and  
 FT M.Fatima Bonaldo."  
 FT /clone="810527"  
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 FT /sex="Female"  
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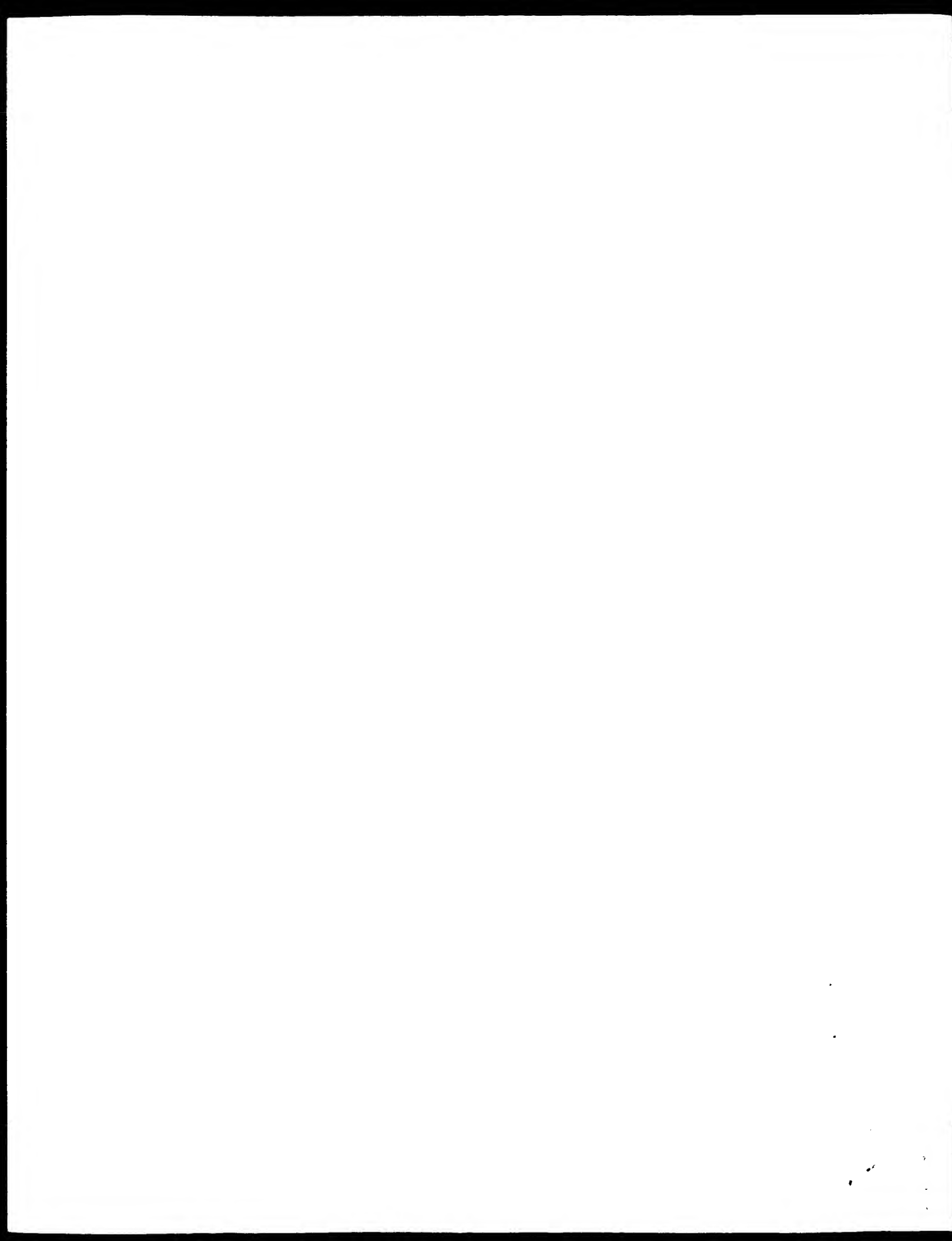
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 QY 73 CAGAGTTTGGTAAACATTTAGTTTGGTATCAGCAGAAACCTGCGCAGGCTCCAGGCTCT 132

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 QY 133 CTCATTATTGGTGGAAACACCAAGCCACTGGTA 166

Search completed: Tue Feb 24 08:31:31 1998  
Job time : 131 secs.

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# WISN

\*\*\*\*\*  
Release 2.10 John F. Collins, BioComputing Research Unit,  
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.  
Distribution rights by IntelliGenetics, Inc.  
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119:EST315

Statistics: Mean 9.844 Variance 1.931 Scale 5.119  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

## SUMMARIES

Result No	Score	Query Match	Length	DR	ID	Description	Prod. No.
1	219	59.5	363	55	AA367405	EST178511 Pancreas tum	0.00e+00
2	210	66.7	328	24	AA295311	EST100471 Pancreas tu	0.00e+00
3	202	64.1	370	24	AA295312	EST100490 Pancreas tu	0.00e+00
4	188	59.7	400	116	AA456778	zw27f11.r1 Soares ova	0.00e+00
5	185	58.7	349	59	AA379044	EST191999 Skin tumor 1	0.00e+00
6	172	54.6	403	53	AA345486	EST151505 Gall bladder	0.00e+00
7	171	54.3	345	26	AA300592	EST13427 Testis tumor	9.19e+29
8	166	52.7	345	26	AA360232	EST16921 Lymph node 1	2.45e+282
9	165	52.4	263	25	AA295341	EST101165 Thymus 111	3.34e+280
10	150	47.6	283	53	AA361872	EST70483 T-cell lymph	5.92e+249
11	146	46.3	218	52	AA381014	EST73787 Thymus 111c	1.21e+247
12	143	45.9	294	55	AA365461	EST77408 Pancreas tum	2.05e+234
13	135	42.9	277	24	AA295377	EST100539 Pancreas tu	7.19e+218
14	130	41.3	244	86	AA320565	zw22b09.r1 Soares ova	1.45e+207
15	129	41.0	280	37	AA327318	EST30586 Colon 1 Hom	1.45e+205
16	127	40.3	255	100	AA292047	zw50312.r1 Soares ova	2.12e+201
17	127	40.3	345	34	AA335386	EST145437 Esophagus tu	2.12e+201
18	126	40.0	264	24	AA295354	EST100123 Pancreas tu	2.40e+199
19	121	38.4	352	27	AA301361	EST14181 Testis tumor	4.21e+189
20	120	38.1	230	87	AA343490	zw27b10.r1 Soares ova	4.67e+187
21	120	38.1	243	99	AA284584	zw22a11.r1 Soares ova	4.67e+187
22	120	38.1	243	83	AA322192	zw31b06.r1 Soares ova	4.67e+187
23	120	38.1	253	100	AA345461	zw30312.r1 Soares ova	4.67e+187
24	120	38.1	355	94	AA294562	zw24503.r1 Soares ova	4.67e+187
25	114	36.2	269	87	AA343031	zw25505.r1 Soares ova	8.03e+175
26	112	35.6	249	79	AA402152	zw55005.r1 Soares ova	9.33e+171
27	112	35.6	357	53	AA361497	EST71040 T-cell lymph	9.33e+171
28	111	35.2	382	25	AA295796	EST100987 Pancreas tu	1.00e+169
29	110	34.9	229	72	AA330371	nc11304.r1 NC1 COAP P	1.07e+166
30	109	34.7	334	37	AA327354	EST135547 Colon 1 Hom	1.29e+162
31	106	33.7	303	26	AA300788	EST13648 Testis tumor	1.33e+158
32	106	33.7	325	33	AA318377	EST20620 Spleen 1 Hom	1.33e+158
33	106	33.7	413	27	AA301347	EST14279 Testis tumor	1.33e+158
34	105	33.3	303	26	AA300891	EST114031 Testis tumor	1.49e+156
35	103	32.4	333	26	AA300732	EST13847 Testis tumor	1.50e+153
36	102	32.4	209	100	AA292350	zw50312.r1 Soares ova	1.55e+150
37	100	31.7	209	100	AA292349	zw50312.r1 Soares ova	1.55e+150
38	95	30.2	301	58	AA277295	EST19917 Small intest	1.67e+136
39	94	29.8	260	71	AA225858	nc27305.r1 NC1 COAP P	1.69e+134
40	93	29.5	292	24	AA295628	EST100951 Pancreas tu	1.63e+132
41	93	28.9	328	33	AA318628	EST30808 Spleen 1 Hom	1.65e+128
42	91	28.9	263	26	AA300451	EST12754 Testis tumor	1.65e+128
43	89	28.3	282	26	AA300401	EST12144 Testis tumor	1.44e+124
44	87	27.6	196	55	AA365524	EST77713 Pancreas tum	1.31e+120
45	86	27.3	299	25	AA325841	EST101050 Pancreas tu	1.39e+118

## ALIGNMENTS

1  
RESULT AA367405 363 bp mRNA EST  
LOCUS EST178511 Pancreas tumor 11: HGT. sapiens chr11: 15,131,347-3  
DEFINITION similar to immunoglobulin kappa light chain.  
ACCESSION AA367405  
NID 92019753  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
Homo.  
REFERENCE 1 (bases 1 to 363)  
AUTHORS Adams, M.D., Keriavage, A.P., Fleischmann, P.D., Fuldner, R.A.,  
Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.C., Gorayne, J.D.,  
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,  
Clayton, P.A., Cline, T.P., Cotton, M.D., Farlie-Hughes, J., Flueckiger,  
Pitzgerald, I.M., Fitzhugh, W.M., Fritchman, J.L., Geachagan, N.S.,  
Glodok, A., Gnehm, C.L., Hanna, W.C., Hedblom, E., Hinkley, P.S., Jr.,

KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
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Mitochondrial eukaryotes: Metazoa: Chordata:  
Vertebrata; Mammalia; Eutheria, Primates, Catarrhini, Hominoidea;  
Homo  
1 (bases 1 to 328)  
ADAMS, M. D., KERLAVAGE, A. R., FLEISCHMANN, R. D., FULDER, R. A.,  
BULT, C. J., LEE, N. H., KIRKNESS, E. F., WEINSTOCK, K. G., GOCAYNE, J. D.,  
WHITE, G., SUTTON, G., BLAKE, J. A., FRANDON, P. C., MAN-NGAI, C.,  
FLAYTON, P. A., CLINE, T. P., COTTON, M. D., EARLE-HUGHES, J., FINE, I. D.,  
FITZGERALD, L. M., FITZBUGH, W. M., FRITZMAN, J. L., GEORGHAKIS, N. S.,  
GLODAS, A., SNEHM, C. L., HANNA, M. C., HEDBLUM, E., HINKLE, P. S., JEFF,  
KELLEY, J. M., KELLEY, J. C., LIU, L.-I., MARMAROS, S. M., MERRICK, J. M.,  
MORENO-PALANQUES, P. F., MCDONALD, I. A., NGUYEN, D. T., PALLERINO, S. M.

**TITLE**  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence

**JOURNAL**  
Nature 377 (6547 Suppl.), 3-174 (1995)

96026280  
Other\_ESTs: THC169106  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers

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Qy	67	GTCAGTTCAGAGTGTGGGTAACTAATTTAGTTTGATATAGATGAATATAGGATC	126			
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Db	232	adggaggtcgggacagaggttcacctctcaacatcagcatctctgagctcgagagatttccc	291
QY	187	AGTGGAGTCTGGGACAGCAATTACCTTCACCTACAGGAGGTTGAGTTCAGAGCAATTGTA	246
Db	292	gtttattactctcagcagctatataaacctgggcatccc	328

QY 247 GTTATTTCTCTCAACACIATAGTACCTGGGGGCA 283

RESULT 3  
LOCUS AA295093 370 bp mRNA EST 18-APP-1997  
DEFINITION EST1004003 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa, variable region (GB:Y00540).  
ACCESSION AA295093  
NID Q1947582  
KEYWORDS EST  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:  
Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:  
Homo.  
REFERENCE 1 (bases 1 to 370)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georhagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,P.F., McDonald,D.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudex,D.M., Shirley,P., Small,K.V., Spriggs,I.A., Tetterback,T.P., Weidman,J.F., Li,Y., Rednath,K.P., Cao,L., Cepeda,M.A., Coleman,I.A., Collins,E.J., Diame,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,P.L., Kunsch,C., Hungjun,J., Li,H., Messner,P., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.  
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (5547 Suppl): 3-174 (1995)  
MEDLINE Q6076280  
COMMENT Other-ESTs: FHC168243  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlavage@igrr.org  
For clone availability, additional sequence and expression information related to this EST, please check the tIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
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Best Local Similarity 86 0% Pred No 0 Gap=00  
Matches 234: Conservative 0 Mismatches 38 Indels 0 Gaps 0

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QY 187 AGTGGSTGGGAGAGAAITCACTCTCAACCAICAGACAGCTGGAGTGGAGACATGGCA 246  
Db 299 gtttattactcagcaacataaagaattgacc 330  
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RESULT 4  
LOCUS AA456778 400 bp mpna EST 06-JUN-1997  
DEFINITION 2427f11.1 Soares ovary tumor NBH01 Homo sapiens cDNA clone 770541 5' similar to gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).  
ACCESSION AA456778  
NID 92177199  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:  
Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:  
Homo.  
REFERENCE 1 (bases 1 to 400)  
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Just,S., Kuraba,T., Lacy,M., Le N., Lennon,G., Marra,M., Martin,J., Moore,R., Schellenberg,K., Steptoe,M., Tan,F., Theising,H., White,F., Wyllie,I., Waterston,P. and Wilson,R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501 St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL: contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Seq primer: -28m3 rev2 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
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/note="Organ: ovary; Vector: pT713D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer: 5'-TGTTACCAATCTGAAGTGGGAGGGGGGGGTTTTTTTTTTTTTTT 3'-, double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."  
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|||||









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QY	67	GCCAGTCCAGAGTGTC--G-GTAAACAATTTAGTGTGTATACGACAAACCTGGCCAGCT	126
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DATA: Human.  
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 1 (bases 1 to 277)  
 Adams, M. D., Kerlavage, A. P., Fleischmann, R. D., Feldner, R. A., Ruit, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gorayze, I., White, O., Sutton, G., Blake, J. A., Brandon, P. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J. C., Fine, L., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geachaden, N. S., Glodex, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jir, Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaro, S. M., Merrick, I., Moreno-Palanges, R. F., McDonald, J. A., Nguyen, P. T., Pellierino, Phillips, C. A., Pyder, S. E., Scott, I. L., Saudek, D. M., Shirley, R. A., Small, K. V., Spriggs, T. A., Utterback, T. P., Weidman, J. E., Wiley, Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dinke, D., Feng, D. F., Farlie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kosak, D. L., Kunsch, C., HungJun, J., Li, H., Weissner, P. S., Olsen Raymond, L., Wei, Y. F., Wang, J., Xu, C., Yu, G. L., Ruben, S. M.,

**TITLE**  
Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence

**JOURNAL**  
Nature 377 (6547 Suppl), 3-174 (1995)

**MEDLINE**  
96026280

**COMMENT**  
Other ESTs: THCL69106  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
4712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423

Fax: 301859423  
 Email: arkerlavet@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human G  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
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 Location/Qualifiers  
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 BASE COUNT  
 ORIGIN





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ORIGIN

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Search completed: Tue Feb 24 08:28:57 1998  
Job time : 150 secs.

\*\*\*\*\*  
W O R L D  
\*\*\*\*\*  
(TM)

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MPsearch\_nu n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 08:20:59 1998. Waspar time 192.49 seconds  
Tabular output not generated.

Title: >US-08-844-215-18  
Description: (1:315) from USC844215.seq  
Percent Score: 915  
N.A. Sequence: 1 CAGCTCAGGAGTTCAGGAGG  
Comp: CTCGAGTCCGTCAGGAGGTCG

Scoring table: TABLE default  
Gap: 1

Nmatch STD : Phase 0: Query 0  
Searched: 55773 seqs, 246912998 bases x 2  
Post-processing: Minimum Match 04  
Listing first 45 summaries

Database: EST-A  
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Statistics: Mean 9.921: Variance 1.934: scale 5.129

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	502	64.1	463.34	R5532	Y182009.11 Homo sapiens	0.000-00
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3	179	55.6	381.58	T91114	EST69430 Homo sapiens	2.180-301
4	173	54.9	383.59	T93916	EST99871 Homo sapiens	2.500-297
5	172	54.6	332.58	T92942	EST77181 Homo sapiens	4.440-295
6	161	51.1	383.58	T27800	EST10007 Homo sapiens	5.260-272
7	141	44.8	361.28	R51922	Y181807.11 Homo sapiens	2.550-230
8	140	44.4	570.34	R70290	Y181808.11 Homo sapiens	3.010-228
9	130	43.2	401.40	R30529	Y181306.11 Homo sapiens	5.790-220
10	124	42.5	360.37	R70297	Y181501.11 Homo sapiens	7.980-216
11	123	42.2	359.64	H27642	Y181497.11 Homo sapiens	9.170-214
12	122	41.9	232.63	H21645	Y183512.11 Homo sapiens	1.060-211
13	131	41.5	299.59	H47498	Y184310.11 Homo sapiens	1.240-209
14	127	40.3	385.64	H25475	Y181905.11 Homo sapiens	2.140-201
15	127	40.3	793.58	T77593	EST100653 Homo sapiens	2.140-201
16	122	38.7	218.64	H77031	Y185301.11 Homo sapiens	3.980-191
17	116	36.8	438.33	P46693	Y182309.11 Homo sapiens	7.590-179
18	108	34.3	171.64	H25498	Y147066.11 Homo sapiens	1.420-162
19	108	34.3	395.58	H25412	EST69484 Homo sapiens	1.420-162
20	108	34.3	447.89	H70726	Y186932.11 Homo sapiens	1.420-162
21	107	34.0	151.63	H22089	Y184005.11 Homo sapiens	1.510-160
22	103	32.7	176.81	H64909	Y184500.11 Homo sapiens	1.480-154
23	101	32.1	516.32	R67559	Y182311.11 Homo sapiens	1.980-148
24	98	31.1	421.27	R48043	Y185031.11 Homo sapiens	2.120-144
25	89	28.3	210.34	R50482	Y183031.11 Homo sapiens	1.070-124
26	89	28.3	330.45	H5841	Y182584.11 Homo sapiens	1.070-124
27	89	28.3	434.11	T91119	Y184007.11 Homo sapiens	1.070-124
28	87	27.6	279.58	T29656	EST89211 Homo sapiens	1.810-120
29	87	27.6	364.58	T97579	EST100649 Homo sapiens	1.810-120
30	86	27.3	235.55	R39891	Y183511.11 Homo sapiens	1.750-118
31	84	26.7	488.64	H57605	Y184805.11 Homo sapiens	1.750-114
32	83	26.3	291.64	H27295	Y183032.11 Homo sapiens	1.420-112
33	83	26.3	470.81	H21115	Y183031.11 Homo sapiens	1.420-112
34	81	25.7	289.58	T77591	EST100107 Homo sapiens	1.200-108
35	80	25.4	289.58	T77721	EST13341 Homo sapiens	1.090-104
36	80	25.4	503.22	R39232	Y183031.11 Homo sapiens	1.090-104
37	76	24.1	397.28	R43771	Y185003.11 Homo sapiens	6.950-99
38	75	23.8	261.27	R46078	Y184403.11 Homo sapiens	6.070-97
39	74	23.5	367.2	T77117	Y181807.11 Homo sapiens	5.260-95
40	74	23.5	387.34	R70292	Y181808.11 Homo sapiens	5.260-95
41	74	23.5	438.34	R60575	Y182310.11 Homo sapiens	5.260-95
42	72	22.9	130.59	H44328	Y184510.11 Homo sapiens	3.840-91
43	68	21.6	366.64	H77048	Y185301.11 Homo sapiens	1.920-83
44	57	21.3	189.51	R93213	Y181310.11 Homo sapiens	1.470-81
45	57	21.3	467.64	H77034	Y185305.11 Homo sapiens	1.470-81

ALIGNMENTS

1 R69532 453 bp mRNA EST 01-JUN-1995  
Y182310.11 Homo sapiens cDNA clone 155249.5, similar to 313M34.4H  
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN)??  
R69532  
G843049  
EST  
human clone=155249 library=Scars breast 2Nbhst vector=pf1140





**6**

<b>RESULT LOCUS DEFINITION</b>	T27870	391 bp	mPNA	FST	06-SEP-1995
	EST19007 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain V region (CR:X06763) (HT-3087).				
<b>ACCESSION</b>	T27870				
<b>NID</b>	9609968				
<b>KEYWORDS</b>	EST.				
<b>SOURCE ORGANISM</b>	Human primer-M13 Reverse library-Human Lung. Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 383)				
<b>PREFERENCE AUTHORS</b>	Adams M.D., Kerlavage A.P., Fleischmann R.D., Fuldner P.A., Bult C.J., Lee N., Kirknes K.E., Weinstock K.G., Socolay J.D., White O., Sutton G., Blake J.A., Brandon P.C., Chiu M.-W., Clayton R.L., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald T.M., FitzHugh W.M., Friedman J.F., Geodharden N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr. P.S., Kiley J.M., Klimke K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palauques P.F., McDonald I.A., Nguyen D.H., Pellegrine S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley P., Small K.V., Springs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins F.J., Dinke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greenleaf M., Gruber J., Hudson P., Kim A., Korak D.L., Kunsch C., Li H., Li H., Meussner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C., Yu G.-L., Zuhlen S.M., Dillon P.J., Fannon M.P., Rosen C.A., Baseltine-Wass A., Fields C., Fraser C.M. and Venter J.C. <b>Initial Assessment of Human Gene Diversity and Expression Patterns</b> Based upon 52 Million Basepairs of cDNA Sequence Unpublished (1995) Other ESTs: THC24452 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tldb.tigr.org				
<b>JOURNAL COMMENT</b>					

<p>For clone availability, additional sequence and expression information related to this EST, please contact the FICR Database (<a href="mailto:tbdinfo@db.tlgr.org">tbdinfo@db.tlgr.org</a>).</p>									
<p>FEATURES</p>									
source	1..383								
	/organism="Homo sapiens"								
mrna	<1..>383								
BASE COUNT	83 a	107 c	101 g	91 t	1 others				
ORIGIN									
	Query Match	51.1%	Score 161;	DB 58;	Length 383;				
	Best Local Similarity:	85.2%	Prod No	5_246-272;					
	Matches 224;	Conservative	0;	Mismatches 34;	Indels	5;	Gaps	3;	
Db	78	ctccagcagccctgtctgtctccaggaggaaagagacccctctctctgcaagcccaatc	137						
QY	14	CTCCAGCTACCTGTGTGTGTCTCCAGGGAAAAAGATTTCTCTCTCTCCAGGGCCAGTC	73						
Db	138	agaggtttaccgcagccctacttagcttggtaccagcaggaadcttgycacagctctcccaaggc	197						
QY	74	AGAGTGT---CGGTAAACAATTAGTTTGSTATCAGCACAAACCTGGCCATGCTCCCAAGC	130						
Db	198	tctctcatctatggtgtcatccagcaggggcactggcatctccagacagatttcaatggcaattg	257						
QY	131	TCTCTATTATTGTTGGAAATACACACAGCAATTTGGTATCTCTAATATTTGATGTTTAAATG	190						
Db	258	ggctcgggcagactctcaactctcaccatccagcggaggttgagctggaaggatttttgcagt	317						
QY	191	GGTCTGGGACAGAAATCTACTTCACATCATGACAGAGCTTCAGATTGTAAGATTTTGCATT	248						



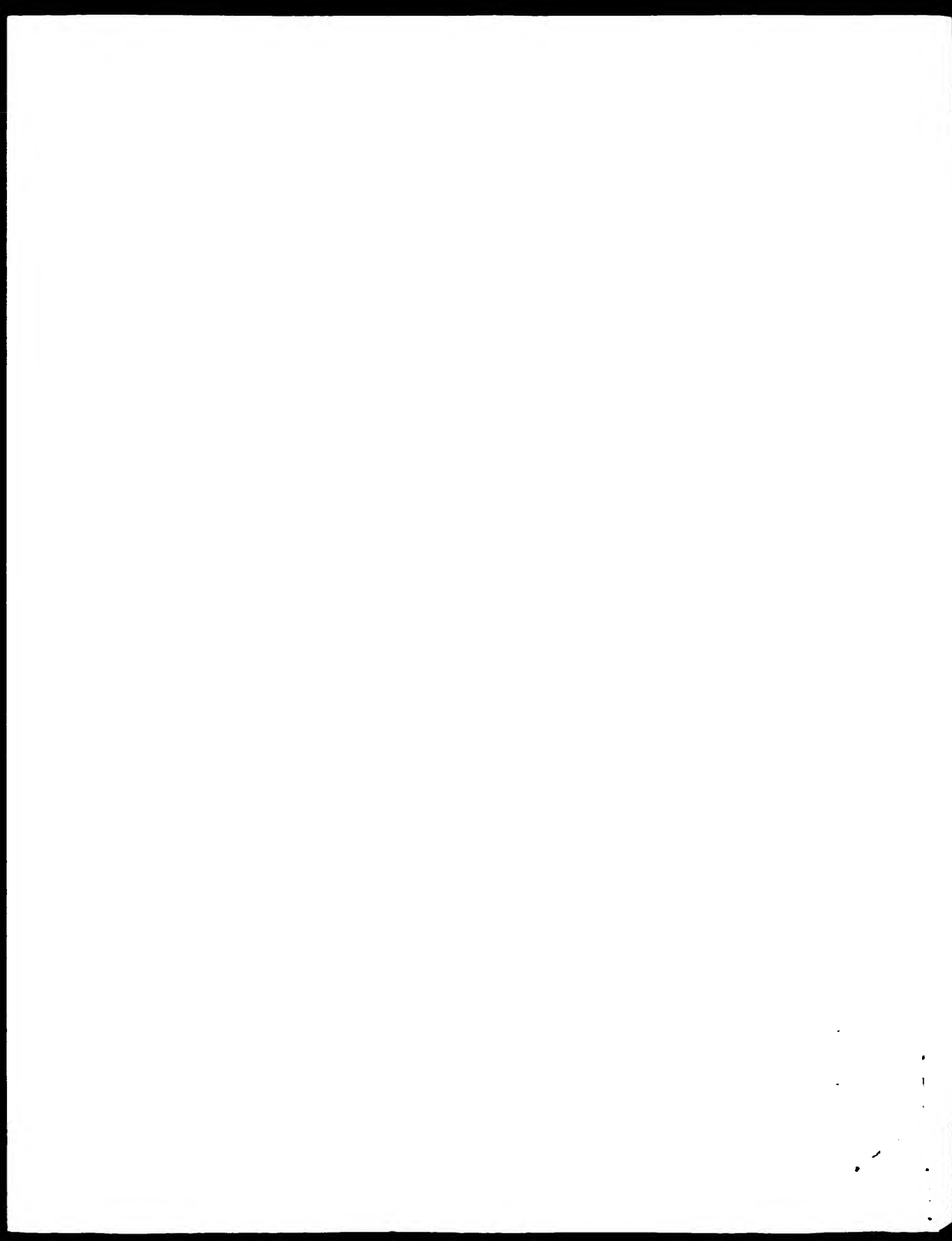
Dn		254	tgggtctgaggacagatttcaatccttcaccattccagcacagtgcgaagcgtagaatattttt 313
QY		189	TGGGTCTGCG-ACAGAATTCACTCT-CACCAT-CAGCAGCTGC-ACTCTGAGCACTTTT- 243
Dn		314	gcagtcatctacttgccagcagtatgatgtagctcacggttcacctcttcgccgcgaaggaa 373
QY		244	GCACTTATTTC-TGTT-CAACTACTATAG-TACCTGCCGCTCATTT-GCG-CGGGGGGA 298
Dn		374	cacaaggt 380 
QY		299	CCAAGTG 305
RESULT	10	R79007	360 bp mpNA EST 09-JUN-1995
Locus DEFINITION		Y185F01.R1 Homo sapiens cDNA clone 146041 5' similar to gb-M12740_cds1 IG KAPPA CHAIN PROTEIN P V-II REGION (HUMAN) :	
ACCESSION		R79007	
NID		q856188	
KEYWORDS		EST.	
SOURCE		human clones=146041 library=Soares placenta Nh2HP vector-BT775D (Pharmacia) With a modified polylinker host=DHI0B (ampicillin resistant) primer=MJ3PPI Psitel=Not I Psite2=Eco RI Female plasma obtained at birth (full term). Ist strand cDNA was primed with Not I - oligo(dT) primer [5]. ACTGCGAACAATCCGGCGCGCAGGAATTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with I and cloned into the Not I and Eco RI sites of the modified pSV vector. Library went through one round of normalization. Libraries constructed by Bento Soares and M.Patina Bonaldo.	
ORGANISM		Homo sapiens Eukaryota; Metazoa; Emetozoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Cloanata; Tetrapoda; Amniota; Mamalia; Theria; Eutheria; Archonta; Primates; Carnivliaui; Hominidae; Homo;	
REFERENCE AUTHORS		1 (bases 1 to 360) Hillier,L., Clark,N., Dubaque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra.M., Parsons,J., Rifkin,L., Rohlfing.T., Soares,M., Tan.F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  The WashU-Merk EST Project Unpublished (1995)	
TITLE JOURNAL COMMENT		Contact: Wilson RK WashU-Merk EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 290 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL : contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information Location/Qualifiers i..360 /organism="Homo sapiens" /clone="146041"	
FEATURES source		81 a 100 c 86 g 88 t 5 others	
BASE COUNT ORIGIN			
Query Match 42.5%; Score 134.; DB 37; Length 360; Best Local Similarity 83.2%; Pred. No. 7.88e+2ib; Matches 193; Conservative 0.; Mismatches 35; Indels 4; Gaps			
Dn		70	ctgacgcag-ctccagcccctgtctgttgtctccagagaagaagtcacccctctctac 128
QY		4	CTCAGCGAGTCTCAGTAACCTTAGTCTGTCAGGGAAAGAGGCTCCCCCTGCTGG 63
Dn		129	agggccagtagaaaatatataaacctgacctggctgtgtaccagcacaaacctggccccag 133











\*\*\*\*\*  
WIREH  
\*\*\*\*\*

Release 2 ID John F. Gallios, BioComputing Research Unit,  
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Distribution rights by IntelliGenetics, Inc.

MPSrch\_nna n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 14 18 48 1998. MacPar time: 19 79 seconds  
Tabular output not generated 732 198 Million cell updates/sec

Title: >US-08-844-215-18  
Description: (1-315) from US08844215.seq  
Perfect Score: 31  
N A Sequence: 1 GAGCTCAGCAGCTCAGC GACCAAGTCGAGTTCAGG 315  
Comp: CCGAGTTCAGCAGCTCAG

Scoring table: TABLE default  
Gap 5

Nmatch STD : Dbase 0: Query 0

Searched: 87931 seqs: 2296021 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-issued  
1-back: 2 51 2 52 4 53 5 54 6 55 7 56 8 PCT96 9 PCT97  
10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Statistics: Mean 7.669. Variance 4 261: scale 1 804

Pred No is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred No.
1	204	64.8	812	7	US-08-053- Sequence 178	Applicat 5 725-132
2	200	63.6	900	7	US-08-053- Sequence 180	Applicat 6 089-129
3	192	61.0	900	7	US-08-053- Sequence 182	Applicat 6 646-123
4	186	59.0	325	11	PCT-US93-1 Sequence 1	Applicat 2 270-118
5	185	58.7	645	12	PCT-US94-0 Sequence 2	Applicat 1 266-117
6	185	58.7	645	13	PCT-US95-1 Sequence 2	Applicat 1 266-117
7	185	58.7	645	7	US-08-300- Sequence 2	Applicat 1 266-117
8	162	51.4	729	7	US-08-276- Sequence 157	Applicat 2 418-100
9	162	51.4	729	13	PCT-US95-0 Sequence 152	Applicat 2 418-100
10	162	51.4	729	13	PCT-US96-0 Sequence 158	Applicat 2 418-100
11	162	51.4	729	7	US-08-276- Sequence 159	Applicat 2 418-100
12	162	51.4	13254	13	US-08-276- Sequence 156	Applicat 2 418-100
13	162	51.4	13254	13	PCT-US95-0 Sequence 156	Applicat 2 418-100
14	162	51.4	13254	13	PCT-US96-0 Sequence 170	Applicat 2 418-100
15	162	51.4	13254	7	US-08-276- Sequence 170	Applicat 2 418-100
16	139	44.1	387	6	US-08-217- Sequence 1	Applicat 3 566-83
17	136	43.2	6238	1	5453363-1 Patent No 5453363	6 948-81
18	132	41.9	318	12	PCT-US94-1 Sequence 2	Applicat 5 618-78
19	132	41.9	318	11	PCT-US93-0 Sequence 3	Applicat 5 618-78

ALIGNMENTS

RESULT 1  
ID US-08-053-131-178 STANDARD: DNA: UNC: 812 BP.

AC XXXXXX  
DI 01-JAN-1900  
DR Sequence 178, Application US/08053131  
CC Sequence 178, Application US/08053131  
CC Patent No. 5661016  
CC GENERAL INFORMATION:  
CC APPLICANT: Lonberg, Nils  
CC APPLICANT: Kay, Robert M  
CC TITLE OF INVENTION: Transgenic N-5661016 Human Animals for  
CC TITLE OF INVENTION: Producing Heterologous Antibodies  
CC NUMBER OF SEQUENCES: 197  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Townsend and Townsend Khourie and Crew  
CC STREET: One Market Plaza, Steuart Tower, Suite 200  
CC CITY: San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94105  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patents: Polaris #2.0. Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER US/08/053,131  
CC FILING DATE: 26-APR-1993  
CC CLASSIFICATION: 800  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/990,860  
CC FILING DATE: 15-DEC-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/810,279  
CC FILING DATE: 17-DEC-1991  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/853,408  
CC FILING DATE: 18-MAR-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,323  
CC REFERENCE/DOCKET NUMBER: 14643-9-3  
CC TELECOMMUNICATION INFORMATION:



CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/053.131  
 CC FILING DATE: 26-APR-1993  
 CC CLASSIFICATION: 800  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/490,860  
 CC FILING DATE: 16-DEC-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/810,279  
 CC FILING DATE: 17-DEC-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/853,408  
 CC FILING DATE: 18-MAR-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Smith, William M.  
 CC REGISTRATION NUMBER: 30,223  
 CC REFERENCE/DOCKET NUMBER: 14643-9-3  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415-326-2400  
 CC TELEFAX: 415-326-2422  
 CC INFORMATION FOR SEQ ID NO: 142:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 900 base pairs  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: DNA (genomic)  
 CC FEATURE:  
 CC NAME/KEY: CDS  
 CC LOCATION: Join(116..163, 351..650)  
 CC Sequence 900 BP: 220 A: 241 C: 201 G: 238 T: 0 other:

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 Best Local Similarity 86.8% Pred No 6,64e-133  
 Matches 244; Conservative 0; Mismatches 34; Indels 3; Gaps 2;  
 Db 375 ACCAGTCTCCAGGACACCGCTCTTTGTTGTCAGGGGAAAGAGACACCTCTCTGTGAGG 434  
 QY 7 ACGAGTCT 66  
 Db 435 GCCAGTCAGAGTGTAGCAGAGCTACTAGCTGTGTACCCAGGACAGAACTGGCCAGGCT 494  
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 QY 244 GCAGTCTATTCTGTCAGCAGATATGGTAGCTTCACTCTCCATCAGCAGACTGGAGCCCT 284

RESULT 4  
 ID PCT-US93-12501-1 STANDARD; DNA: UNC: 325 BP.  
 AC XXXXX  
 DT 01-JAN-1900  
 DE Sequence 1, Application PC/TUS9312501.  
 CC Sequence 1, Application PC/TUS9312501.  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Chang, Ise Wen  
 CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IgA MONOCLONAL ANTIBODIES AND  
 CC TITLE OF INVENTION: RELATED PRODUCTS FOR ALLERGY TREATMENT  
 CC NUMBER OF SEQUENCES: 10  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Tanox Biosystems, Inc.  
 CC STREET: 10301 Stella Link Rd.  
 CC CITY: Houston  
 CC STATE: Texas

CC COUNTRY: USA  
 CC ZIP: 77025  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5" Hi Density Diskette  
 CC COMPUTER: IBM PS/2  
 CC OPERATING SYSTEM: IFS, Version 4.0  
 CC SOFTWARE: Wordperfect 5.1  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US93/12501  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER:  
 CC FILING DATE:  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Mirabel, Eric P.  
 CC REGISTRATION NUMBER: 31,211  
 CC REFERENCE/DOCKET NUMBER: TNX92-3  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 713-664-2288  
 CC TELEFAX: 713-664-8914  
 CC INFORMATION FOR SEQ ID NO: 1:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 325 nucleotides  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: double stranded  
 CC TOPOLOGY: Linear  
 CC FEATURE:  
 CC Sequence 325 BP: 79 A: 93 C: 79 G: 74 T: 0 other:

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 Matches 256; Conservative 0; Mismatches 52; Indels 3; Gaps 2;  
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 QY 7 ACGAGTCT 66  
 Db 73 GCCAGTCAGAGTGTAGCAGAGCTACTAGCTGTGTAACTAAGAGCACTGGAGATCTAGGCT 132  
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 QY 244 GCAGTGTATTCTGTCAGCAGATATGGTAGCTTCACTCTCCATCAGCAGACTGGAGCCCTGA 303  
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RESULT 5  
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 AC XXXXX  
 DT 01-JAN-1900  
 DE Sequence 2, Application PC/TUS9401258.  
 CC Sequence 2, Application PC/TUS9401258.  
 CC GENERAL INFORMATION:  
 CC APPLICANT:  
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
 CC TITLE OF INVENTION: USING UNIVERSAL OP RANDOMIZED IMMUNOGENIC LIBRARIES  
 CC CHAINS  
 CC NUMBER OF SEQUENCES: 61  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible





CHAINS

CC NUMBER OF SEQUENCES: 70  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: The Scripps Research Institute  
CC STREET: 10566 No 564798th Torrey Pines Road, 1P28  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent in Release #1 0, Version #1 25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/300.386A  
CC FILING DATE: 02-SEP-1994  
CC CLASSIFICATION: 41c  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/174,674  
CC FILING DATE: 28-DEC-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/826,523  
CC FILING DATE: 27-JAN-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/454,148  
CC FILING DATE: 30-SEP-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/012,555  
CC FILING DATE: 02-FEB-1994  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: TSP1 409.1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-554-2937  
CC TELEFAX: 619-554-6312  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 645 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
SQ Sequence 646 BP: 162 A: 187 C: 170 G: 127 I: 0 other:

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Best Local Similarity 85.5%; Pred. No. 1.26e-117;  
Matches 241; Conservative 0; Mismatches 38; Indels 3; Gaps 1;  
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Db 61 TCAGGAGGAGAGCAGCAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCC 120  
QY 61 TCAGGAGGAGAGCAGCAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCC 117  
Db 121 CAGGCTCCAGGAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCC 180  
QY 118 CAGGCTCCAGGAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCC 177  
Db 181 TCAGGAGGAGAGCAGCAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCC 240  
QY 178 TCAGGAGGAGAGCAGCAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCC 237  
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RESULT

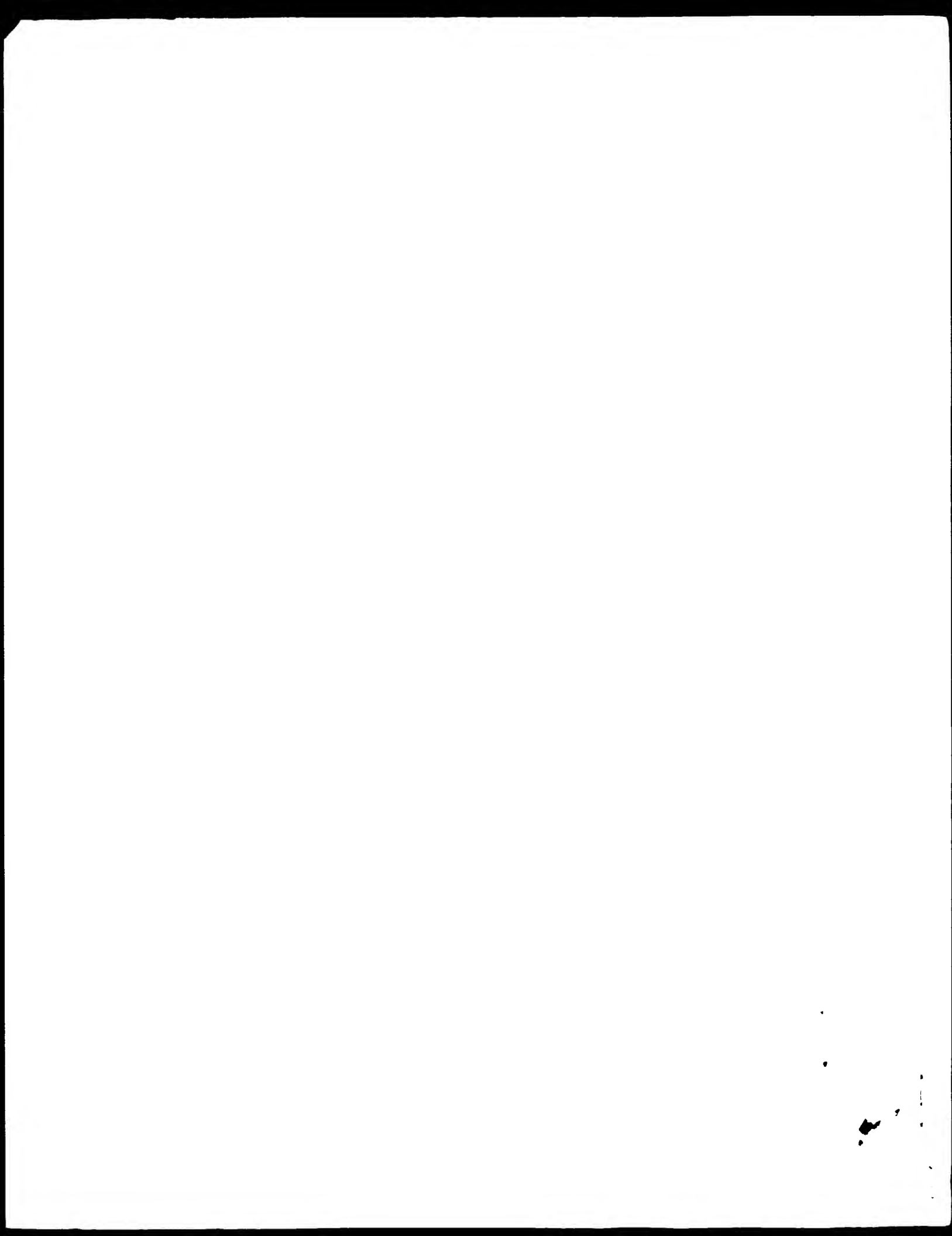
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AC xxxxxx  
DT 01-JAN-1900  
UE Sequence 152, Application US/08276852.  
CC Sequence 152, Application US/08276852  
CC Patent No. 5652138  
CC GENERAL INFORMATION:  
CC APPLICANT: Burton, Dennis R  
CC APPLICANT: Barbas, Carlos F  
CC APPLICANT: Lerner, Richard A  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: The Scripps Research Institute, Office of  
CC ADDRESSEE: Patent Counsel  
CC STREET: 10666 No 5652138th Torrey Pines Road, Suite 220.  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent in Release #1 0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/276,852  
CC FILING DATE: 18-JUL-1994  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/178,302  
CC FILING DATE: 30-SEP-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/954,148  
CC FILING DATE: 30-SEP-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: TSP1452P  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-554-2937  
CC TELEFAX: 619-554-6312  
CC INFORMATION FOR SEQ ID NO: 152:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 729 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 9..715  
SQ Sequence 729 BP: 173 A: 208 C: 192 G: 156 I: 0 other:  
Query Match 51.4%; Score 162; DB 7; Length 729;  
Best Local Similarity 78.6%; Pred. No. 2.41e-100;  
Matches 243; Conservative 0; Mismatches 53; Indels 3; Gaps 2;  
Db 78 CTCAGCGAGTCTCCAGGACCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCTGT 197  
QY 4 CTCAGGAGTCTCCAGGACCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCTGT 64  
Db 138 AGGTCAGCTCAGCAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCTGT 197  
QY 64 AGGTCAGCTCAGCAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCTGT 120  
Db 198 GTCAGGAGGAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCTGT 287  
QY 198 GTCAGGAGGAGCTCTGTTTGTCTCCAGGGAAGAGGACCTCTCTGT 186







Search completed: Tue Feb 24 14:19:44 1998  
Job time : 55 secs.











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Db 253 gcaagtgggtctggacagacttcaactctcaccatcagcagactggagccctgagatttt 312
QY 184 GGCAGTGGGTCTGGACAGAAATTCACCTCACCATCAGCAGCTTSCASTCTGAGGACTTT 243
Db 313 gcaagtattactcagcagatggtacatccacgtacacattttgcccagggaccacag 372
QY 244 GCAGITTTATTTCTGTCAACACTATAGTACCTGGCCGTCACTTTTCGGCGGGGACCAAG 303

RESULT 6
ID Q78853 standard; DNA; 900 BP.
AC Q78853;
DE 10-JUN-1995 (first entry)
DE Human V-kappa gene vk55.5.
KW Transgenic mouse; transgenic animal; antibody engineering;
KW variable region; light chain; minilocus transgene;
KW chimeric antibody; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 180..593
FT /tag= a
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Query Match 63.5%; Score 200; DB 12; Length 900.
Best Local Similarity 86.0%; Pred. No. 5.19e-116;
Matches 239; Conservative 0; Mismatches 39; Indels 0; Gaps 0.

Db 421 acacagctctccagccacctgtctgtctccagggaaagaccacccctctctcagc 480
QY 7 ACCAGCTCTCCAGCCAGCTGTCTGTCTCCAGGGGAAAGAGCTCTCTCTCTGAGG 66
Db 541 aggcctctctatgatgatccaaagggccactggcctcagcagcaggttcagtgcc 600
QY 127 AGGCTCTCTATTTATGTTGTAACACCTAGAGCCACCTGTAACAGAGAGCTTCCAGTGGC 186
Db 601 agtgggctctggacagactctcactctcaccatcagcagccttagagcctgaattttgca 660
QY 187 AGTGGGCTCTGGACAGAAATTCATCTCACCATCAGCAGCTTSCASTCTGAGGACTTTTSCA 246

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Db 661 gttattactgtagaggtgtagcaactggtgacatccacac 698
QY 247 GTTATTCTGTGCAACACTATAGTACCTGGCGCTCAC 284

RESULT 7
ID Q44223 standard; DNA; 900 BP.
AC Q44223;
DE 10-NOV-1993 (first entry)
DE Human DNA fragment vk65.5 containing V-kappa gene segment.
KW Immunoglobulin; light chain variable region; minilocus;
KW isotype switching; unrearranged functional Vκ gene segment;
KW human light chain transgene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_signal 119..126
FT /tag= a
FT /note= "Splicing and recombination signal ?"
FT misc_recomb 696..723
FT /tag= b
FT /note= "Splicing and recombination signal sequence"
FT exon 180..228
FT /tag= c
FT /number= 1
FT /note= "nucleotides 180-182 represent the
FT initiation codon, i.e. the start of the ORF;
FT the precise start point of the exon is not
FT indicated"
FT intron 229..397
FT /tag= d
FT /number= 1
FT /tag= e
FT /note= "ORF not terminated by a stop codon"
FT W0931227-A.
PD 24-JUN-1993.
PR 17-DEC-1992; U10983.
PR 17-DEC-1991; US-810279.
PR 18-MAR-1992; US-853408.
PR 23-JUN-1992; US-904068.
PA (GENP-) GENPHARM INT INC.
PI Kay RM, Lonberg N;
DP WPI: 93-214169/26.
DR P-PSDB: R38649.
PT Transgenic non-human animals contg. immunoglobulin heavy chain
PT transgene - used to produce useful antibodies by isotype
PT switching
PS Example 21; Fig 42; 196pp; English.
CC The V-kappa specific oligonucleotide Q50327 was used to probe a
CC human placental genomic DNA library cloned into lambdaEMBL3/SpeI/T7.
CC DNA fragments containing V-kappa segments from positive phase
CC clones were subcloned into plasmid vectors. Variable gene segments
CC from the resulting clones were sequenced and functional clones were
CC selected on the basis of open reading frames, intact donor and
CC acceptor splice sites and intact recombination sequences. The
CC sequences obtained from four different plasmid clones were
CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44223-244225,
CC respectively).
SQ Sequence 900 BP; 225 A; 244 C; 254 G; 227 T;

Query Match 63.5%; Score 200; DB 7; Length 900;
Best Local Similarity 86.0%; Pred. No. 5.19e-116;
Matches 239; Conservative 0; Mismatches 39; Indels 0; Gaps 0.

Db 421 acacagctctccagccacctgtctgtctccagggaaagaccacccctctctcagc 480
QY 7 ACCAGCTCTCCAGCCAGCTGTCTGTCTCCAGGGGAAAGAGCTCTCTCTCTGAGG 66
Db 481 gccagtcagggatgttagcagactacttagcgtggtacacagcagacaggtgccc 540
QY 67 GCCAGTCAGAGTGTGCGTAACAAATTTAGCTTGTATCAGCAGAAATCTGCTAGGCTTCCC 126

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## RESULT

PA (BRIM)

Dδ	871	atgaggctcgggcacacactccactccattccaccagcaacacataagaatgaatttaca	930
Qγ	187	AGTGGTGCTGGGACCAAAATTCATTATCCATCACATACAGCGGTGCAGTTTGAAGACTTGGTA	246
Dδ	931	gtttattactgctcaaacac	948
Qγ	247	GTTATTCTGTCAAGC	264

RESULT    10  
 IE         cDNA; standard: cUNA; 1242 BP.  
 AC         OI1878:  
 DT         OI-AYG-1991  
 DE         DE 1B1 IGG aberrant light chain clone 4ng/Vx15.  
 KW         Immunoglobulin G; light chain; variable regions; duplication.

KW passive immunity: group B streptococci; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..49  
 FT /tag= a  
 FT /note= "leader"  
 FT misc\_RNA 50..388  
 FT /tag= b  
 FT /label= L'V 1  
 FT /note= "encodes last 3 amino acids of leader and the rearranged VJ gene"  
 FT misc\_RNA 389..726  
 FT /tag= c  
 FT /label= L'V 2  
 FT /note= "encodes last 3 amino acids of leader and the rearranged VJ gene"  
 FT misc\_RNA 728..1044  
 FT /tag= d  
 FT /note= "constant region"  
 FT polyA\_signal 1221..1225  
 FT /tag= e  
 PN W09106305-A.  
 PD 16-MAY-1991.  
 PE 06-NOV-1990: U06426.  
 PR 07-NOV-1989: US-432700  
 PA (RPM ) RPISTOL-MYERS SQUID  
 PI Shuford WW, Harris LJ, Raff HV;  
 DR WPI: 91-163947/22.  
 DR P-PSDB: R12128.  
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -  
 PT formed by duplicating esp. variable region of light chain of IgG  
 PT class  
 PS Claim 42: Fig 16. 104pp. English.  
 CC This sequence encodes an aberrant light chain containing two L'V  
 CC regions. Antibody molecules of the invention can include one or two  
 CC such aberrant light chains to produce heavier antibodies. These  
 CC heavier antibodies were found to have higher avidity than antibodies  
 CC with just a single copy of the L'V region. The clone is not  
 CC complete; it starts with the 5' of the ATG initiator codon.  
 CC See also Q11879 and Q11880.  
 SQ Sequence 1242 BP; 291 A; 383 C, 302 G, 266 T.  
 Query Match 63.5%; Score 200; DB 2; Length 1242;  
 Best Local Similarity 88.8%; Pred. No 5 19e-116;  
 Matches 229; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 Db 71 acaaatctccagcaccctcttcttctccaggggaagagccaccctctctcaggg 130  
 QY 7 AGCGAGTCTCCAGGACCCCTGTCTGTCTCCAGGGGAAAGAGGCTCCCTCTCAGG 66  
 Db 131 gccagtcagagtggtggcag;tacttagcctggf'accaacagaaacctgcccggctccc 190  
 QY 67 GCCAGTCAGAGTGTGGTAACAAATTAGCTTGGTATCAGCAGAAACCTGGCCAGGCTCCC 126  
 Db 191 aggcacctcatatgatgcattcccaacaggggccactggcatcccgccaggttcagtgcc 250  
 QY 127 AGGCTCTCATTTATGGTGGAAACACAGACGACCTGTTACCCAGACAGGTTTCAGTGGC 186  
 Db 251 atgggtctggagagacttcaactctcaactcagcagcctagagcctgaagattttgca 310  
 QY 187 AGTGGGCTGSSGACAAATTAATCACTCTCACTATCAAGCCCTGAGCCCTGAGGACTTTGCA 246  
 Db 311 gttattactgtcaaac 328  
 QY 247 GTTTATTCTGTCAACAC 264  
 RESULT 11  
 ID Q49155 standard: cDNA; 387 BP.  
 AC Q49155;  
 DT 21-NOV-1993 (first entry)  
 DE Fl05-rearranged variable region light chain.  
 KW Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;

KW CD4; receptor; hybridoma; polymerase chain reaction: PCR; heavy; light;  
 KW chain; epitope; immune deficiency; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..57  
 FT /tag= a  
 FT mat\_peptide 58..387  
 FT /tag= b  
 FN W09312232-A.  
 PD 24-JUN-1993.  
 PE 10-DEC-1992: U10928.  
 PR 10-DEC-1991: US-804552.  
 PA (DAND ) DANA FARBER CANCER INST INC  
 PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL CORP.  
 PI Haseltine WA, Marasco WA, Posner MP, Sedroski JG;  
 DR WPI: 93-214174/26.  
 DR P-PSDB: R41286.  
 PT DNA segments encoding monoclonal antibody - which binds to gp120  
 PT and neutralises HIV, for treating AIDS, and for diagnosing and  
 PT monitoring HIV infection  
 PS Claim 1; Page 79; 109pp; English.  
 CC mRNA from the known hybridoma F105 was converted to cDNA and this  
 CC subjected to PCR amplification using primers corresp. to appropriate  
 CC parts of the heavy or light chains and having restriction sites to  
 CC permit cloning. The extension products were isolated and sequenced.  
 CC The recombinant human monoclonal antibody (MAB) binds to a  
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks  
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad  
 CC range of HIV isolates. The MAB may be used to treat immune  
 CC deficiency, esp. at doses of 0.1-10 mg/kg.  
 SQ Sequence 387 BP; 88 A; 111 C; 101 G; 87 T;  
 Query Match 62.2%; Score 196; DB 7; Length 387;  
 Best Local Similarity 83.9%; Pred. No 2.89e-113;  
 Matches 261; Conservative 0; Mismatches 47; Indels 3; Gaps 2;  
 Db 73 acgcagtcctcagcaccctcttctgtctgcaggggaagagccaccctctctcaggg 132  
 QY 7 AGCGAGTCTCCAGGACCCCTGTCTGTCTCCAGGGGAAAGAGGCTCCCTCTCAGG 66  
 Db 133 gccagtcagagtggttagcagcaggttacttagctgtaccagcaaaacctgaccacct 192  
 QY 67 GCCAGTCAGAGTGTGGTAACAA-T---TAGCTTGTGTATCAGCAGAAACCTCCAGGCT 123  
 Db 133 gccagtcctctctctatgtatgtatcagcaggggacagtcagtcagtcagtcagtcagtc 252  
 QY 124 CCCAGGCTCTCTCAITTAAGGAGGAAACACACAGAGACACAGAGAGAGAGAGAGAGAG 183  
 Db 253 gccagtcgggtctgggacagagacttcactctcaccatcagcagagtgagagcctaaagatttt 312  
 QY 184 GGCAGTGGGCTGGGACAGAGATTCACCTTCACATATCAGTACAGTACAGTACAGTACAGT 243  
 Db 313 gccagtcattactgtcagcgaatgatataactcagttgtactcttggccagggagcccaag 372  
 QY 244 GCAGTTATTCTGTCAACACTATAGTACTGTCGCGCTCCTCTCTCTCTCTCTCTCTCTCT 303  
 Db 373 ctggagatcaa 383  
 QY 304 GTCAGTTCAA 314  
 RESULT 12  
 ID Q42707 standard, DNA, 390 BP.  
 AC Q42707;  
 DT 01-NOV-1993 (first entry)  
 DE Fl05VK-F105Jk.  
 KW Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;  
 KW CD4; receptor; hybridoma; polymerase chain reaction: PCR; heavy; light;  
 KW chain; epitope; immune deficiency; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /tag= a



ID Q78854 standard; DNA: 900 BP.  
 AC Q78854;  
 DE 07-JUN-1995 (first entry)  
 DE Human V-kappa gene vk65.8.  
 KW Transgenic mouse; transgenic animal; antibody engineering;  
 KW variable region; light chain; minilocus transgene;  
 KW chimeric antibody; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT exon 116..650  
 FT CDS  
 FT /tag= a 163..350  
 FT intron b  
 FT /tag= b 163..350  
 FT misc\_signal 653..659  
 FT /tag= c  
 FT /label= Splicing\_signal  
 FT misc\_signal 672..680  
 FT /tag= d  
 FT /label= Recombination\_signal  
 PN W09425595-A.  
 PD 10-NOV-1994.  
 PE 25-APR-1994; U04580.  
 PR 26-APR-1993; US-053131.  
 PR 22-JUL-1993; US-066762.  
 PR 18-NOV-1993; US-155301.  
 PR 03-DEC-1993; US-161739.  
 PR 10-DEC-1993; US-165699.  
 PR 09-MAR-1994; US-209741.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N;  
 DR WPI: 94-358263/44.  
 DR P-PSDB: P62930.  
 PT Transgenic non-human animals producing heterologous or chimeric  
 PT antibodies - for binding a pre-determined human antigen with  
 PT increased affinity  
 PS Disclosure, Fig. 43, 295pp, English.  
 CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in  
 CC Q78852-Q78855, respectively) each contain a V-kappa gene segment  
 CC that can be used to form a complete human light chain minilocus  
 CC transgene for expression in a nonhuman transgenic animal for  
 CC heterologous antibody production. The deduced amino acid  
 CC sequences of the V-kappa coding regions are given in P62928-P62931  
 SQ Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;  
 Query Match 61.0%; Score 192; DB 12; Length 900;  
 Best Local Similarity 86.8%; Pred No 1 60e-110; Mismatches 34; Indels 3; Gaps 2;  
 Matches 244, Conservative 0, Mismatches 34, Indels 3, Gaps 2;  
 Db 375 acgcagctccagcagccctgtctgtctccaggggaagagccacccctctcgcagg 434  
 QY 7 ACCGAGTCTCCAGCAGCCCTGTCTGTCTCCAGGGGAAAGAGCCCTCTCTGCGAGG 66  
 Db 435 gccagtcagagtgtagcagcagctacttagcctgtgtaccagcaggaacacctgcccagct 494  
 QY 67 GCCAGTCAGAGTGTGGTAACAA-T--TTAGCTTGTGTATCAGCAGAAACCTGCGCAGGCT 123  
 Db 495 cccagctcctcatctatgtgtccacagcagggccactgcatccaccagaggttcaqt 554  
 QY 124 CCCAGGCTCTCATIIAUGGIGGNAACACACAGAGCTACGGTACCCACACAGGTTCACT 183  
 Db 555 gccagtggtgtggagcagacttctcctccatccagcagactggagcctgaagatttt 614  
 QY 184 GGCAGTGGGTCTGGGACAGAAATTCATCTCATTACCAACAGAGGCTGACGACGACTTT 243  
 Db 615 gccagtgattactgacagctatgtagtcaactccacc 655  
 QY 244 GCAGTTATTCTGTCAACTACTATAGTACCTGGCGGCTCAC 284  
 Search completed: Tue Feb 24 09:20:24 1998  
 Job time : 88 secs.

DE DNA fragment vk65.8, containing variable kappa chain gene.  
 KW variable; kappa chain; gene segment; human; DNA fragment; vk65.8;  
 KW unrearranged; light chain; minilocus; transgene; transgenic; mouse;  
 OS production; heterologous; antibody; gamma, immunoglobulin; ss.  
 FH Homo sapiens.  
 FH Key Location/Qualifiers  
 FT exon 116..164  
 FT /tag= a 352..650  
 FT /tag= b  
 PN US5545806-A.  
 PD 13-AUG-1996. 574748.  
 PE 29-AUG-1990; US-574748.  
 PR 29-AUG-1990; US-575962.  
 PR 31-AUG-1991; US-810279.  
 PR 17-DEC-1991; US-853408.  
 PR 18-MAR-1992; US-904068.  
 PR 23-JUN-1992; US-990860.  
 PR 16-DEC-1992; US-990860.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N;  
 DR WPI: 96-383736/38.  
 DR P-PSDB: W03948.  
 PT Prodn. of heterologous human immunoglobulin(s) - by immunising  
 PT transgenic mice  
 PS Example 21; Fig 43; 94pp; English.  
 CC The present sequence is the variable kappa chain gene segment  
 CC containing human DNA fragment, vk65.8, which was co-injected along  
 CC with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half  
 CC day mouse embryo pronuclei, to generate an unrearranged light chain  
 CC minilocus transgene. The resulting transgenic mice can be used for  
 CC the production of heterologous (i.e. human) antibodies against  
 CC specific antigens, this comprises immunising a mouse with a  
 CC preselected antigen and collecting antigen binding heterologous  
 CC human gamma immunoglobulins.  
 SQ Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;  
 Query Match 61.0%; Score 192; DB 47; Length 900;  
 Best Local Similarity 86.8%; Pred No 1 60e-110; Mismatches 34; Indels 3; Gaps 2;  
 Matches 244, Conservative 0, Mismatches 34, Indels 3, Gaps 2;  
 Db 375 acgcagctccagcagccctgtctgtctccaggggaagagccacccctctcgcagg 434  
 QY 7 ACCGAGTCTCCAGCAGCCCTGTCTGTCTCCAGGGGAAAGAGCCCTCTCTGCGAGG 66  
 Db 435 gccagtcagagtgtagcagcagctacttagcctgtgtaccagcaggaacacctgcccagct 494  
 QY 67 GCCAGTCAGAGTGTGGTAACAA-T--TTAGCTTGTGTATCAGCAGAAACCTGCGCAGGCT 123  
 Db 495 cccagctcctcatctatgtgtccacagcagggccactgcatccaccagaggttcaqt 554  
 QY 124 CCCAGGCTCTCATIIAUGGIGGNAACACACAGAGCTACGGTACCCACACAGGTTCACT 183  
 Db 555 gccagtggtgtggagcagacttctcctccatccagcagactggagcctgaagatttt 614  
 QY 184 GGCAGTGGGTCTGGGACAGAAATTCATCTCATTACCAACAGAGGCTGACGACGACTTT 243  
 Db 615 gccagtgattactgacagctatgtagtcaactccacc 655  
 QY 244 GCAGTTATTCTGTCAACTACTATAGTACCTGGCGGCTCAC 284  
 Search completed: Tue Feb 24 09:20:24 1998  
 Job time : 88 secs.

RESULT 15  
 ID 37182 standard; DNA: 900 BP.  
 AC T3742.  
 DT 14-APR-1997 (first entry)

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Statistics:      Mean 9.849;  Variance 1.939;  scale 5.079

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

Result      Query
No.  Score  Match Length DB  ID  Description  Pred. No.
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1  255    83  5    100  50  HS1244890  ZW0711.11  Scores Ave  0.00E+00
2  237    74  5     419  30  AAC115149  ZW0709.51  Not_Guar_L  0.00E+00

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ALIGNMENTS

RESULT 1

ID HS1244850 standard: RNA; EST: 400 BP.

AC AA456778;

NI 92177199

DT 07-JUN-1997 (Rel. 52, Created)

DT 07-JUN-1997 (Rel. 52, Last updated, Version 1)

EE 58772111 Soares et al., 1997, Nucleic Acids Res. 25: 10541

EE 58772111 Soares et al., 1997, Nucleic Acids Res. 25: 10541

DE \* similar to gb:X06764.10 KAPPA CHAIN PRECURSOR V-JII REGION

DE (HUMAN)??

DE EST.

OS Homo sapiens (human)

OS Eukaryotae: mitochondrial eukaryotes, Metazoa, Chordata:

OC Vertebrata: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

RN [1]

RP 1-400

RP Hillier L., Allen M., Bowles T., Dubucq T., Geisel G., Gest S.,

RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,

RA Moore B., Schellenberg K., Stepien M., Tan F., Weising B.,

RA White Y., Wyllie T., Waterston P., Wilson P.

RI "WashU-Merck EST Project 1997";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@washington.westnet.edu this clone is available royalty free through

CC ILNU - contact the IMAGE Consortium (info@image.llnwd.net) for





RT Tumor Gene Index:  
 RL Unpublished  
 CC Contact: Robert Strausberg Ph.D. Tel: (301) 466-1560 Email:  
 CC Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,  
 CC M.D., Michael P. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:  
 CC David R. Krizman, Ph.D. cDNA Library Arrayed by Greg Lennon, Ph.D.  
 CC DNA Sequencing by: Washington University Genome Sequencing Center  
 CC Clone Distribution: NCI-CGAP clone distribution information can be  
 CC found through the I M A G E Consortium/LLNL at:  
 CC www.biol.nsl.gov/ibrrp/image/image.html Insert Length: 1070 Std  
 CC Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality  
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 FT 1..418  
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 FT /note="vector: pAMP10; mRNA made from liposarcoma, cDNA  
 FT made by oligo-dT priming. Non-directionally cloned.  
 FT Size-selected on agarose gel, average insert size 600 bp  
 FT Reference: Krizman et al (1996) Cancer Research  
 FT 56:5380-5383.  
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 FT /lab\_host="DH10B"  
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 Best Local Similarity 98.8% Pred. No. 0.00e+00;  
 Matches 277; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

Db 95 agcagctctccagcagcctctctctctctccaggggaagagccaccctctctcagg 154  
 QY 7 AGCGAGGCTCCAGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 66  
 Db 155 gccatccagatcatcatcagcagccccccttagccctgggtatcagcaaaacccctggccaggt 214  
 QY 67 GCGATCCAGAGTGTATGAGAGAACTATGATTTAGCTTGGTACGAGCAAAACCTTGGCTAGGCT 126  
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 QY 247 GCGAGGCTCCAGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306  
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 AC AA479857  
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 DT 23-JUN-1997 (rel 52, Created)  
 DE 23-JUN-1997 (rel 52, Last updated, Version 1)  
 DE z35b05.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone 739953  
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 KW EST:  
 OS Homo sapiens (human)  
 OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea;  
 RN [1]  
 RP 1-242  
 RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,  
 Krizman D., Kuraba T., Lacy M., Lennon G., Maizumi M.,

RA Krizman D., Kuraba T., Lacy M., Lennon G., Maizumi M.,  
 RA Martin J., Moore B., Schellenberg K., Steptoe M., Tan P.,  
 RA Thaising H., White Y., Wyllie T., Waterston P., Wilson R.,  
 RL "WashU-NCI human EST Project";  
 CC Contact: Wilson PK Washington University School of Medicine 4444  
 CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 266  
 CC 1800 Fax: 314 266 Email: est@wustl.edu This clone is  
 CC available royalty-free through LLNL; contact the IMAGE Consortium  
 CC (infoimage@llnl.gov) for further information. Seq primer: -28ml3  
 CC rev2 ET from Amersham.  
 PH Key Location/Qualifiers  
 FT source  
 FT 1..242  
 FT /organism="Homo sapiens"  
 FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a  
 FT modified polylinker; Site: 1; Not 1; Site: 2; Eco RI; 1st  
 FT strand cDNA was primed with a Not 1 - oligo(dT) primer [5'  
 FT TGTTACCAATCTCAAGTGGAGGCGGCGGGTGTGTGTGTGTGTGTGTGTGTGTGT  
 FT double-stranded cDNA was size selected, ligated to Eco RI  
 FT adapters (Pharmacia), digested with Not 1 and cloned into  
 FT the Not 1 and Eco RI sites of a modified pT73 vector  
 FT (Pharmacia). Library constructed by Bento Soares and  
 FT M. Fatima Bonaldo."  
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 FT /tissue\_type="ovarian tumor"  
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 Query Match 66.4% Score 211; DB 64; Length 242;  
 Best Local Similarity 94.6% Pred. No. 0.00e+00;  
 Matches 225; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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 Db 121 gacaaattct 180  
 QY 191 GCGATCCAGAGTGTATGAGAGAACTATGATTTAGCTTGGTACGAGCAAAACCTTGGCTAGGCT 249  
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 QY 310 GA 311

RESULT 5  
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 DEFINITION z35b05.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone 739953  
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 (HUMAN);  
 ACCESSION AA479857  
 NID 92205743  
 KEYWORDS EST  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
 REFERENCE 1 (bases 1 to 242)  
 AUTHORS Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,  
 Krizman D., Kuraba T., Lacy M., Lennon G., Maizumi M.,

Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,  
White Y., Wylie T., Waterston P., Wilson P.;  
"WashU-Merck EST Project 1997";  
Unpublished.  
Contact: Wilson PK WashU-Merck EST Project, Washington University  
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
waterston@wustl.edu This cDNA is available royalty-free through  
LLNL; contact the IMAGE Consortium ([info@imgl.gov](mailto:info@imgl.gov)) for  
further information. Seq primer: -38ml3 rev2 ET from Amersham.  
Key Location/Qualifiers

Key	Location/Qualifiers
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FT	/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT	modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
FT	strand cDNA was primed with a Not I - oligo(dT) primer [5
FT	IGTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTT 3'],
FT	double-stranded cDNA was size selected, ligated to Eco RI
FT	adapters (Pharmacia), digested with Not I and cloned into
FT	the Not I and Eco RI sites of a modified pT73 vector
FT	(Pharmacia). Library constructed by Bento Soares and
FT	M.Fatima Ronaldo."
FT	/clone="770329"
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FT	<1..>269
FT	mRNA
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[illegible]

1 (bases 1 to 171)

REFERENCE

ANTHOPS

Krillman, D., Allen, M., Bowles, I., Dubuque, T., Gaisel, C., Iost, S., Krizman, L., Krabat, T., Lacy, M., Le, N., Lennon, C., Marri, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, P., and Wilson, P.

TITLE

WASHU-NCI human EST Project

UNPUBLISHED (1997)

JOURNAL

TITLE WashU-NCI human EST Project  
JOURNAL Unpublished (1997)





[illegible]

mRNA

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QY 7 ACCAGATGTCAGGACGCTGCTTGGTCTCCAGGGGAAAGAGGCGACGCTGCTGCGG 66
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Db 213 cccagactccatctatatagatccatccaggagcgcacacccacacacacacacacac 262
QY 127 CCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 177

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Search completed: Tue Feb 24 08:08:45 1998  
 Job time : 174 secs.

100





Submitted (18-FEB-1997) Division of Molecular Immunology,  
Department of Pathology, Cornell University Medical College, 1300







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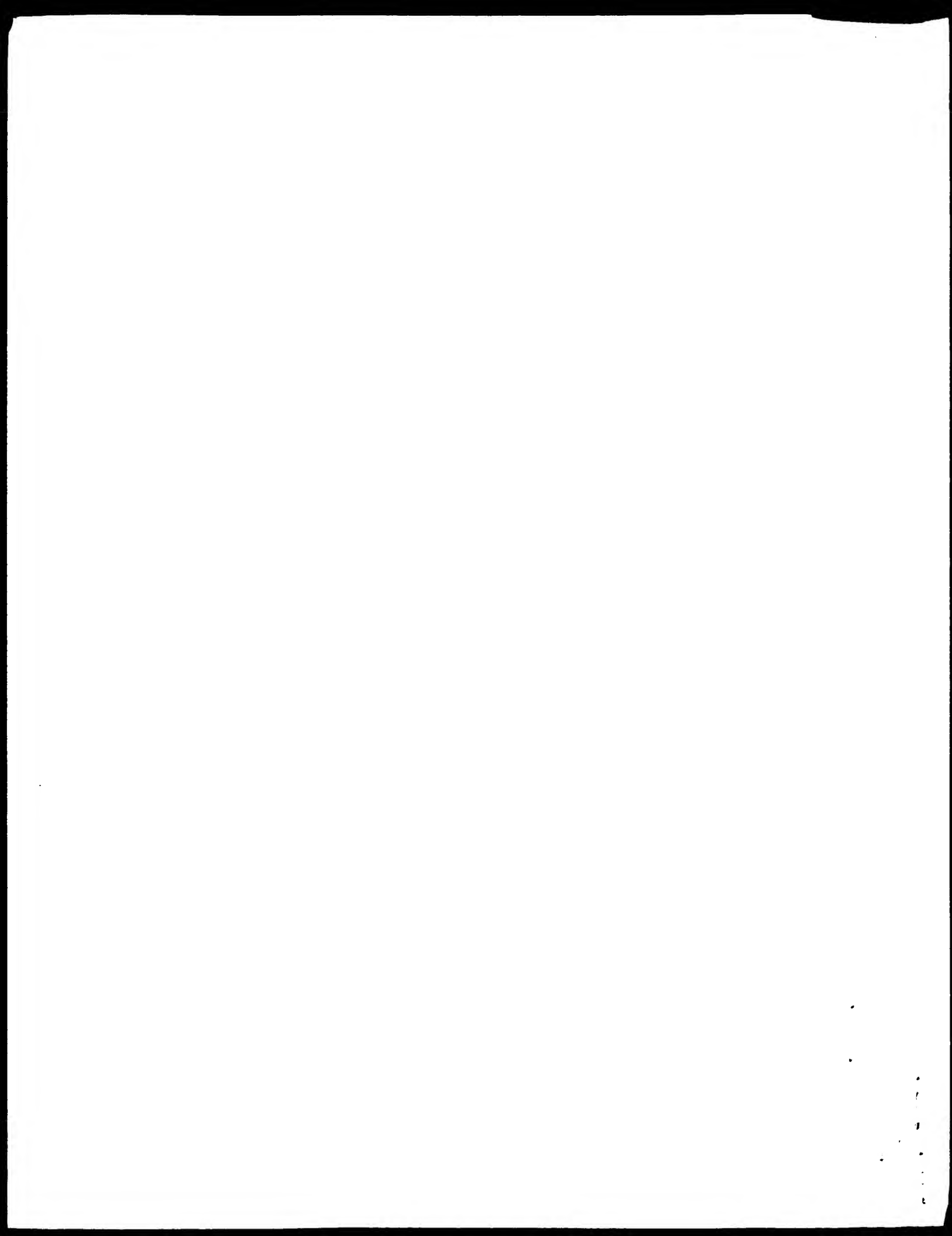
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BASE COUNT	78 a	90 c	85 a	71 f











\*\*\*\*\*

# WQERLEH

(TM)

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993, 1994, 1995 University of Edinburgh, UK  
Distribution Rights by IntelliGenetics, Inc.  
MPsearch\_nnn n.a. - n.a database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 09:02:42 1998 Maspar 1000 100 50 seconds  
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Comp: : TCGAGTGGCTGAGAGAGGCTTC : GCTTGGCTGAGAGAGGCTTC 119

Scoring table: TABLE default  
Gap 5  
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Searched: 397346 seqs, 141010104 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

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7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208  
13:EST209 14:EST210 15:EST211 16:EST212 17:EST213  
18:EST214 19:EST215 20:EST216 21:EST217 22:EST218  
23:EST219 24:EST220 25:EST221 26:EST222 27:EST223  
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58:EST254 59:EST255 60:EST256 61:EST257 62:EST258  
63:EST259 64:EST260 65:EST261 66:EST262 67:EST263  
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119:EST315

Statistics: Mean 9.839: Variance 1.925: scale 5.110  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description	Prod. No.
1	266	83.6	400	116	AA456778	247711 T-Cell lymph
2	255	80.2	346	26	AA300582	EST13457 Testis tumor
3	249	78.3	349	59	AA379044	EST19199 Skin tumor
4	242	76.1	403	73	AA345486	EST15105 Gall bladder
5	237	74.5	402	52	AA350223	EST19341 Lymph node
6	227	65.1	328	24	AA295311	EST100471 Pancreas tu
7	193	60.7	370	24	AA295093	EST100400 Pancreas tu
8	186	58.5	363	55	AA367405	EST178511 Pancreas tu
9	182	57.2	277	24	AA295377	EST120538 Pancreas tu
10	178	56.0	284	37	AA327218	EST10585 Colon I Homo
11	177	55.7	253	25	AA295941	EST101165 Thymus I
12	174	54.7	294	55	AA366461	EST17408 Pancreas tum
13	173	54.4	264	24	AA295154	EST100323 Pancreas tu
14	161	50.6	269	87	AA434001	EST5501 T-Cell lymph
15	147	46.3	269	100	AA344662	EST101165 Thymus I
16	146	45.9	283	53	AA361678	EST17083 T-cell lymph
17	145	45.5	209	100	AA292499	EST101165 Thymus I
18	142	44.7	238	62	AA383014	EST17787 Thymus I
19	135	42.5	260	71	AA225858	EST17083 T-cell lymph
20	134	39.0	230	97	AA341290	EST17083 T-cell lymph
21	134	39.0	243	83	AA422182	EST17083 T-cell lymph
22	134	39.0	243	83	AA422182	EST17083 T-cell lymph
23	134	39.0	243	83	AA422182	EST17083 T-cell lymph
24	132	38.4	244	86	AA430565	EST17083 T-cell lymph
25	132	38.4	255	99	AA284552	EST13847 Testis tumor
26	132	38.4	345	39	AA335086	EST17408 Pancreas tum
27	130	37.7	253	100	AA292499	EST101165 Thymus I
28	119	37.4	255	100	AA292499	EST101165 Thymus I
29	118	37.1	413	37	AA301347	EST14379 Testis tumor
30	116	36.5	335	33	AA318377	EST120620 Spleen I Hom
31	114	35.8	352	27	AA301461	EST14381 Testis tumor
32	112	35.2	249	79	AA402152	EST5005 T-Cell lymph
33	109	34.3	357	53	AA361497	EST17040 T-cell lymph
34	107	33.6	442	80	AA405415	EST5602 T-Cell lymph
35	106	33.3	382	25	AA295786	EST100987 Pancreas tu
36	104	32.7	322	72	AA320271	EST13504 Testis tumor
37	102	32.1	374	37	AA327254	EST17083 T-cell lymph
38	99	31.1	363	26	AA300551	EST13704 Testis tumor
39	96	30.2	303	26	AA300789	EST13704 Testis tumor
40	96	30.2	398	94	AA423447	EST17083 T-cell lymph
41	95	29.9	249	92	AA419046	EST17083 T-cell lymph
42	95	29.9	248	85	AA430449	EST17083 T-cell lymph
43	95	29.9	248	85	AA430449	EST17083 T-cell lymph
44	95	29.9	303	26	AA300789	EST13704 Testis tumor
45	91	28.5	324	33	AA318377	EST120620 Spleen I Hom

## ALIGNMENTS

RESULT 1 AA456778 400 bp MPRA EST 06-JUN-1997  
LOCUS 247711 T-Cell lymph HOMO sapiens cDNA clone 247711  
DEFINITION 247711 T-Cell lymph HOMO sapiens cDNA clone 247711  
ACCESSION AA456778  
NID 92177199  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotic; Mitochondrial; eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;  
Homo  
REFERENCE 1 (bases 1 to 400)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubaque, J., Geisel, G., Jost, S.,  
Kucabay, T., Lacy, M., Le, N., Lennon, G., Martin, M.,  
Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theisinger, B.,  
White, Y., Wylie, J., Waterston, R. and Wilson, R.  
TITLE WashU-Merck EST Project 1997





mrna	<1..>403	86 a	113 c	107 g	93 t	4 others
BASE COUNT						
ORIGIN						
Query Match	76.1%;	Score 242;	DB 73;	Length 403;		
Best Local Similarity	92.9%;	Pred. No. 0.00e+00;				
Matches	262;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;	
Db	42	ccaggggaagagccctctctcgcagggccagtcagcgtgttagcagcagtcactta	101			
Qy	37	CCAGGGGAAAGACCCACCTCTCTCTGCGGGCCAGTCAGAGTGTAGGAGCAACTACTTA	96			
Db	102	gcctgtatcagcagaaaacctggcagagctcccaggtctccatctatgtgtgcctcagg	161			
Qy	97	GCCTGTATCAGCAAAACCTGCGCAGGCTCCAGGCTCCATCTATATGTTATCCAGC	156			
Db	162	agggccactggcctccacagaggttcagtcagtcagtcagtcagtcagtcagtcctc	221			
Qy	157	AGGGCCACTGGATCCACAGAGTTCAGTGCAGTGGTCTGGACAGAGTTCACATCTC	216			
Db	222	accatcagcagactggagctgaagattttgcagtcgtattactgtcagcagtcagtcag	281			
Qy	217	ACCATCAGCAGCTGGAGCTGAAGATTTTGCAGTCTATTACTGTACAGTATGCTAGC	276			
Db	282	tcacttagacgttcggccagaggaagtcagtcagtcagtcagtcagtcagtcagtc	323			
Qy	277	TCACCTCGGACTTTTGGCCAGGGACCAAGTTGGAGATCAAA	318			
RESULT	5					
LOCUS	AA360223	405 bp	mrna	EST	21-APR-1997	
DEFINITION	EST69341 Lymph node I Homo sapiens cDNA 5' end similar to					
ACCESSION	AA360223					
NID	92012543					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 405)					
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudet, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Paymond, I., Wei, Y.F., Wing, J., Xu, C., Yu, G.I., Ruben, S.M., Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.					
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence					
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)					
MEDLINE	96026280					
COMMENT	Contact: Kerlavage, AP Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: 'arkerlav@tigr.org' For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene					
FEATURES						
source	Location/Qualifiers					
1..405	/organism="Homo sapiens"					
	/note="Organ: lymph node; Vector: pBluescript SK-; Site: 1"					
	ECORI; Site: 2: XhoI"					
	/clone_lib="Lymph node I"					
	/dev_stage="adult"					
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ORIGIN						
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Best Local Similarity	92.6%;	Pred. No. 0.00e+00;				
Matches	250;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;	
Db	92	etccagggcaacctgtcttctctaggggaacacagcaccctctctcgcagggccagtc	151			
Qy	14	CTCCAGGCAACCTGTCTTGTCTCCAGGGGAAGAGTCACTCTCTCTCTCTCTCTCT	73			
Db	152	agactgttagagagctctctcttagcctgggtacccagcagaacctggccaggtcccccagc	211			
Qy	74	AGAGTGTTAGAGCAACTACTTACCTGCTGCTAGCAGTAAAGATTTGGTATCTCTCTCT	133			
Db	212	tcctcatctatgtgctccagcagggccactggccatcccccagcaggttcagtcagtcag	271			
Qy	134	TCTCTATCTATGTTGTATCCAGGAGGCCCTGCTATCCAGACAGGTTCAGTGGTAGT	193			
Db	272	ggcttggcagacttactnctcancatcagcagcagcagcagcagcagcagcagcagcagc	331			
Qy	194	GGTCTGGGACAGACTTCT	253			
Db	332	attactgtcaatgttatgttagtcacacac	361			
Qy	254	ATTACTGTACAGCAGTATGTTAGTCACTCCTC	283			
RESULT	6					
LOCUS	AA295311	328 bp	mrna	EST	18-APR-1997	
DEFINITION	EST100471 Pancreas tumor I Homo sapiens cDNA 5' end similar to					
ACCESSION	AA295311					
NID	91947646					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 328)					
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudet, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Paymond, I., Wei, Y.F., Wing, J., Xu, C., Yu, G.I., Ruben, S.M., Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.					
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence					
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)					
MEDLINE	96026280					
COMMENT	Other_ESTs: THC169106					

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Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
source  
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/organism="Homo sapiens"  
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/dev\_stage="adult"  
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Matches 243; Conservative 0; Mismatches 25; Indels 3; Gaps 1.  
5b 52 acgcaantnagcaccctctctgtgtntccagggaagagcaccctctctcagg 111  
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QY 7 AGCGAGTCCAGAGACCTGCTGTTGCTCCAGGAGAGACCTCTCTCTGAGG 66  
112 gccatccagatgttagcagcaact---tagcctgtgtaccagcagaacacctggccagct 168  
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QY 67 GCGAGTCAGAGTGTAGAGGCAAGTACCTGAGTGGTACAGAGAGAGAGAGAGAGT 126  
169 cccagagct 228  
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QY 127 CCGAGGCT 186  
229 gccatgggtctgagcagatctcactctcancatcagcctctcagctctgagatctt 288  
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QY 187 GCGATGAGTGTAG 246  
289 ncagtttattactgcagcagatataataact 319  
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QY 247 GCAGGTATTACTGTCAGCAGTATGCTAGCT 277

RESULT 7 AA295093 370 bp mRNA EST 18-APR-1997  
LOCUS EST000000 Pancreas tumor I Homo sapiens cDNA 5' end similar to  
DEFINITION similar to immunoglobulin kappa variable region (GB:Y00540).  
ACCESSION AA295093  
NID 91947582  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Hominoidea;  
Homo.  
REFERENCE 1 (bases 1 to 370)  
AUTHORS Adams M.D., Kerlavage A.P., Fleischmann P.D., Fuldner R.A.,  
Burt C.J., Lee N.H., Kirkness E.F., Weinstock K.G., Gockayne J.D.,  
White O., Sutton G., Blake J.A., Brandon P.C., Man-Wai C.,  
Clayton P.A., Cline J.P., Cotton M.D., Earle-Hughes E., Fine L.D.,  
Fitzgerald T.M., Fitzhugh W.M., Fritchman J.L., Georghiou N.S.,  
Glock A., Guelm C.L., Hanna M.C., Hedden E., Hinkle P.S., J.  
Kelley J.M., Kelley J.C., Liu L.-I., Marmaro S.M., Merrick J.M.,  
Moreno-Palancas R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,  
Phillips C.A., Ryder S.E., Scott J.L., Saudet D.M., Shirley R.,  
Small K.V., Spriggs T.A., Terback T.P., Weidman J.F., Li Y.,  
Bednarek P.P., Cao J., Cepeda M.A., Coleman T.A., Collins E.J.,  
Dimick D., Feng D.-F., Fertle A., Fischer C., Hastings G.A.,  
He W.W., Hu T.S., Greene J.M., Gruber T., Hudson P., Kim A.K.,

Kozak D.L., Kupsch C., Hungate J., Li H., Meisner P.S., Olsen B.,  
Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Rubin S.M.,  
Dillon P.J., Fannon M.R., Rosen C.A., Rosette W.A., Fields C.,  
Fraser C.M. and Venter J.C.  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
Other ESTs: TC0169243  
Contact: Kerlavage, AP  
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Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
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/note="Organ: pancreas; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
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/dev\_stage="adult"  
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Query Match 60.7% Score 193; DB 24; Length 370;  
Best Local Similarity 88.8%; Pred No. 0.00e+00;  
Matches 231; Conservative 0; Mismatches 26; Indels 3; Gaps 1.  
5b 59 acgcantnccagcaccctctctgtntccagggaagagcaccctctctcagca 118  
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QY 7 AGCGAGTCCAGAGACCTGCTGTTGCTCCAGGAGAGACCTCTCTCTGAGG 66  
119 gccatccagatgttagcagcaact---tagcctgtgtaccagcagaacacctggccagca 175  
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QY 67 GCGAGTCAGAGTGTAGAGGCAAGTACCTGAGTGGTACAGAGAGAGAGAGAGAGT 126  
176 cccagct 235  
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QY 127 CCGAGGCT 186  
236 gccatgggtctgagcagatctcactctcancatcagcctctcagctctgagatctt 245  
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QY 187 GCGATGAGTGTAG 246  
296 gcagtttattactgcagca 315  
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QY 247 GCAGGTATTACTGTCAGCAGTATGCTAGCT 266

RESULT 8 AA367405 363 bp mRNA EST 21-APR-1997  
LOCUS EST078511 Pancreas tumor III Homo sapiens cDNA 5' end similar to  
DEFINITION similar to immunoglobulin kappa light chain.  
ACCESSION AA367405  
NID 92019753  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Hominoidea;  
Homo.  
REFERENCE 1 (bases 1 to 363)  
AUTHORS Adams M.D., Kerlavage A.P., Fleischmann P.D., Fuldner R.A.,  
Burt C.J., Lee N.H., Kirkness E.F., Weinstock K.G., Gockayne J.D.,  
White O., Sutton G., Blake J.A., Brandon P.C., Man-Wai C.,  
Clayton P.A., Cline J.P., Cotton M.D., Earle-Hughes E., Fine L.D.,  
Fitzgerald T.M., Fitzhugh W.M., Fritchman J.L., Georghiou N.S.,  
Glock A., Guelm C.L., Hanna M.C., Hedden E., Hinkle P.S., J.  
Kelley J.M., Kelley J.C., Liu L.-I., Marmaro S.M., Merrick J.M.,  
Moreno-Palancas R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,  
Phillips C.A., Ryder S.E., Scott J.L., Saudet D.M., Shirley R.,  
Small K.V., Spriggs T.A., Terback T.P., Weidman J.F., Li Y.,  
Bednarek P.P., Cao J., Cepeda M.A., Coleman T.A., Collins E.J.,  
Dimick D., Feng D.-F., Fertle A., Fischer C., Hastings G.A.,  
He W.W., Hu T.S., Greene J.M., Gruber T., Hudson P., Kim A.K.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, I.R., Weidman, J.F., Li, Y., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
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96026280

Contact: Kerlavage, AR  
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The Institute for Genomic Research  
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Fax: 3018699423  
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
Source  
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EcoRI; Site\_2: XhoI"  
/clone\_lib="Pancreas tumor III"  
/dev\_stage="adult"  
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mpna  
BASE COUNT 74 a 108 c 90 g 88 t 3 others  
ORIGIN

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Best Local Similarity 82.9%; Pred. NO. 0.00e+00;  
Matches 252; Conservative 0; Mismatches 49; Indels 3; Gaps 3;  
Db 1 ctccacaccctgtctgtctcagaggaaagagtcacccctctcagagccagtc 60  
QY 14 CTCACGGACCTGTCTTGTCTCCAGGGGAAAGAGGACGCTCTCTCTGCGGGCCAGTC 73  
Db 61 agagtttgta-cgt-t-cttagcctgtatcagcacaaacctggcgaacctccagcc 117  
QY 74 AGAGTGTAGGACCACTACTTAGCTGTATGCTGTACGACCAAAACCTGGCCAGGCTCCACGGC 133  
Db 118 tctctatcatggtgtgtccacagggccactggtactccggccacaccttcagtgccggtg 177  
QY 134 TCTCATATATGTTATCTAGCAGGAGGCTACTTGGCATCCCATATAGTTAGTGGTACTG 193  
Db 178 ggtctagacgaacttcaactccaccatcagcgccctcagctcgtgaggaactttgcagtat 237  
QY 194 GGTCTGGGACACATCTACTCTCACCATCAGCAGACTGGACCCCTGAAGATTTTGCATGT 253  
Db 238 actattgtagcagtagtatataactggcctctcaacttttcggcgaggagaccacagtagaga 297  
QY 254 ATTACTGTACGAGTAGTATGTTAGTCTACCTCGGACTTTTGGCCAGGGGACCAAGTTGGAGA 313  
Db 298 teaa 301  
QY 314 TCAA 317

RESULT 9 AA295377 277 bp mpna EST 18-APR-1997  
LOCUS EST100538 Pancreas tumor I Homo sapiens cDNA 5' end similar to  
DEFINITION immunoglobulin kappa light chain, VJ regions.

AA295377  
gi1947711  
EST  
KEYWORDS  
SOURCE  
Homo sapiens  
ORGANISM

REFERENCE  
AUTHORS  
1. (bases 1 to 277)  
Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,

Rult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.D., Fritchman, J.L., Geoghagen, N.S., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Hedblom, E., Hinkle, P.S., Jr., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, I.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

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Nature 377 (6547 Suppl), 3-174 (1995)  
96026280

COMMENT  
Other ESTs: THG169106  
Contact: Kerlavage, AR  
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The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423

Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
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/note="Organ: pancreas; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
/clone\_lib="Pancreas tumor I"  
/dev\_stage="adult"  
^1..277  
BASE COUNT 56 a 83 c 70 g 61 t 7 others  
ORIGIN

FEATURES  
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/note="Organ: pancreas; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
/clone\_lib="Pancreas tumor I"  
/dev\_stage="adult"  
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Query Match 57.2%; Score 182; DB 54; Length 277;  
Best Local Similarity 93.8%; Pred. No. 6.00e-06;  
Matches 196; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
Db 70 acgagcttcacagcacccctgtttgttccagggggaagagccacctctccagcag 129  
QY 7 ACCGAGTCTCAGGACCCCTCTTTGTCTCCAGGGGAAAGAGGACGCTCTCTCTGCGGGCCAGTC 166  
Db 130 gccagtcagagtgtagcagcagctacttagctggtaccagcagaacctcagcagcagct 189  
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Db 190 cccagntccctcatctatggtgcacaggggagccactggnatccacagaggttcagt 249  
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QY 187 GSCATGCGGCTCGGACAGACTTTCACCTCT 215









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Db 47 ctccaggcaccctgtcttctccagggqaaagagccaccctctctctgagggccagtc 106
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Db 167 tctcatctatggtgcatccagcagggccactgg-atcccagac 209
QY 134 TCCTCATCTATGTGTATCCAGCAGGCGCCACTGGCATCCAGAC 177

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Search completed: Tue Feb 24 08:05:25 1998  
 Job time : 162 secs.

# WIRELL (TM)

\*\*\*\*\*  
Release 2.0 John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.  
Distribution rights by Intelligentics, Inc.  
\*\*\*\*\*  
MPsrch\_nna n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:27:00 Mar 98 Wap: time 210.58 seconds  
745.741 Million cell updates/sec  
Tabular output not generated.  
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Description: (1-318) from "G09044111 seq  
Perfect score: 318  
N.A. Sequence: 1 GAGUACAGGAGAGUACAGG GAGUACAGGAGAGUACAGG  
Comp: GAGUACAGGAGAGUACAGG GAGUACAGGAGAGUACAGG  
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Scoring table:  
Gap 0  
Nmatch STD : Dbase 0: Query 0  
Searched: 665703 seqs, 246912800 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
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## Statistics

Mean: 9.876, Variance: 1.923, scale: 5.136

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	253	77.6	381	58	T29114	EST59430 Homo sapiens	0.00e+00
2	247	77.7	383	59	T29216	EST59871 Homo sapiens	0.00e+00
3	219	68.9	383	58	T27870	EST19007 Homo sapiens	0.00e+00
4	206	64.8	570	34	T70220	Y51908 r1 Homo sapiens	0.00e+00
5	203	63.8	401	40	P10529	Y51906 r1 Homo sapiens	0.00e+00
6	195	61.3	394	69	H44768	Y24410 r1 Homo sapiens	0.00e+00
7	191	60.1	463	34	P69532	Y52506 r1 Homo sapiens	0.00e+00
8	194	57.9	222	52	T22342	EST7191 Homo sapiens	0.00e+00
9	184	57.9	359	64	H27642	Y51907 r1 Homo sapiens	0.00e+00
10	166	52.2	451	10	T90236	Y51910 r1 Homo sapiens	4.14e-24
11	153	48.1	438	33	P64693	Y52509 r1 Homo sapiens	7.13e-256
12	151	47.5	171	64	H54458	Y51916 r1 Homo sapiens	1.67e-251
13	138	43.4	385	64	H26475	Y51905 r1 Homo sapiens	1.21e-224
14	137	43.1	421	27	R48043	Y51901 r1 Homo sapiens	1.44e-222
15	132	41.5	351	28	P51922	Y51907 r1 Homo sapiens	2.22e-212
16	130	40.9	393	58	T27592	EST19053 Homo sapiens	4.25e-208
17	128	40.3	360	37	H79907	Y51901 r1 Homo sapiens	5.93e-204
18	120	37.7	232	63	H21645	Y51912 r1 Homo sapiens	1.65e-187
19	119	37.4	225	65	H29891	Y51911 r1 Homo sapiens	1.85e-186
20	118	37.1	201	54	H26286	Y51902 r1 Homo sapiens	2.07e-183
21	118	37.1	470	81	H21115	Y51901 r1 Homo sapiens	2.07e-183
22	113	35.5	218	64	H27031	Y51901 r1 Homo sapiens	3.42e-173
23	109	34.3	270	59	T29456	EST89211 Homo sapiens	4.77e-165
24	102	32.1	434	11	T91179	Y51907 r1 Homo sapiens	7.26e-151
25	101	31.8	130	60	H44329	Y51910 r1 Homo sapiens	7.57e-149
26	101	31.8	251	63	H22088	Y51905 r1 Homo sapiens	7.57e-149
27	98	30.1	503	22	P28232	EST59384 Homo sapiens	8.11e-145
28	98	30.8	295	58	T29112	EST59384 Homo sapiens	8.33e-144
29	97	30.5	264	59	T27570	EST19049 Homo sapiens	8.51e-141
30	96	30.2	176	81	H64909	Y51910 r1 Homo sapiens	8.65e-139
31	94	30.2	516	23	P67559	Y51911 r1 Homo sapiens	8.65e-139
32	94	30.6	390	45	H56841	Y51914 r1 Homo sapiens	8.79e-135
33	92	28.9	210	34	P24422	Y51903 r1 Homo sapiens	8.74e-131
34	91	28.6	447	89	H70726	Y51912 r1 Homo sapiens	8.54e-129
35	88	27.7	397	28	P43771	Y51901 r1 Homo sapiens	8.04e-123
36	88	27.7	489	64	H35635	Y51905 r1 Homo sapiens	8.04e-123
37	87	27.4	261	27	H38788	Y51903 r1 Homo sapiens	7.76e-121
38	87	27.4	392	6	T29111	EST59384 Homo sapiens	7.76e-121
39	84	26.1	439	34	P50537	Y51902 r1 Homo sapiens	6.68e-110
40	81	25.5	366	64	H27048	Y51916 r1 Homo sapiens	5.41e-109
41	80	25.2	409	52	P69036	Y51907 r1 Homo sapiens	4.96e-107
42	78	24.5	467	54	H27034	Y51901 r1 Homo sapiens	4.96e-107
43	76	23.9	350	58	T27587	EST19047 Homo sapiens	3.26e-99
44	75	23.6	298	59	T27581	EST19017 Homo sapiens	2.87e-97
45	75	23.6	307	34	P70202	Y51903 r1 Homo sapiens	2.87e-97

## ALIGNMENTS

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RESULT T29114 381 bp mRNA EST 06-SEP-1997  
LOCUS EST59430 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V(III). J(V) regions (GB:227170) (H13121).  
DEFINITION T29114  
ACCESSION T29114  
NID g61122  
KEYWORDS EST.  
human primer-M13 Reverse library Human lymphoid tissue.

9612014  
 EST.  
 human primer-M13 Reverse library-Human Pancreas.  
 Homo sapiens  
 Organism  
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata, Vertebrata, Gnathostomata, Osteichthyes,  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 383)  
 Adams,M.D., Kerlavage,A.P., Fleischmann,R.P., Fuldner,P.A.,  
 Bult,C.J., Lee,N., Kirkness,F.F., Weinstock,K.G., Gorvayne,J.D.,  
 White,C., Sutton,G., Blake,J.A., Brandon,P.C., Chiu,M.-W.,  
 Clayton,P.A., Cline,P.T., Cotton,M.D., Earle-Hughes,E., Fine,L.B.,  
 Fitzgerald,L.M., Fitzhugh,W.M.C., Fritchman,J.L., Geodhagen,N.S.M.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,  
 Kelley,J.M., Kline,M.K., Kelley,J.C., Liu,T.-I., Marmaros,S.M.,  
 Merrick,J.M., Moreno-Palmarques,R.F., McDonald,I.A., Nguyen,B.T.,  
 Pellegrino,S.M., Phillips,C.A., Pyder,S.E., Scott,L.,  
 Saudke,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Tutterback,T.R.,  
 Weidman,J.F., Li,Y., Sedmak,D.P., Cao,L., Repeda,M.A.,  
 Coleman,T.A., Collins,E.J., Dinko,D., Feng,P., Ferrie,A.,  
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
 Meissner,P.S., Olson,H., Raymond,I., Wei,Y.-F., Wing,J., Xu,C.,  
 Yu,G.-L., Pfen,S.M., Dillon,P.J., Fannon,M.F., Rosen,C.A.,  
 Baseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
 Initial Assessment of Human Gene Diversity and Expression Patterns  
 Based Upon 52 Million Basepairs of cDNA Sequence  
 Unpublished (1995)

JOURNAL: *Journal of Molecular Evolution*  
 COMMENT: Based Upon 52 Million Basepairs of cDNA Sequence  
 Unpublished (1995)  
 Contact: Venter, JC  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@db.tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact the TIGR Database  
 (tdbinfo@db.tigr.org).  
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 Db 111 gccagtcagagtggttagcaacaactaactagcctgtaccagcagcaaacctgccacagnt 170  
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 QY 67 GCGAGTCAGAGTGTTAGGAGGCAACTACTTACCTCTGGTAGTAGTAAAAATGGCCAGGCT 126  
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 Db 171 ccagatctctcatctatggttacatccatcagggcactggcactccagacaggttcagt 230  
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 QY 127 CCAGGCTCCCTCATCTATGTTGTATCCAGCAGGGCCACTGSCATCCACAGAGSITCAGT 186  
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 Db 231 ggcagtgggctgggacagagctttcaactcttgaccatccagcagactggagccctgaagatt 290  
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 QY 187 GGCAGTGGGTCTGGGACAAAGATTTCATCTTCTATCATCAGTCAGAGCTGAGAGCTCAAGATT 244  
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 Db 291 ttgcagtgattatctgctcagcagatagtgtagctcacggggagaggtttgcagcagggagcc 350  
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 QY 245 TT-GCAGTGTATTACTGTGCAGCAGATAGTGTAAGCTACCTCGAGATTTTGGGCTAGGGGACC 303  
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 Db 351 aagdtgggaagtcaa 364  
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 QY 304 AAGTTGGAGATCAA 317



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Db 393 acagtgaataataaaa 408
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QY 304 A-AGTTGGAGATCAAA 318
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RESULT 5 R10529 401 bp mRNA EST 06-APR-1995
LOCUS Yf31a06.r1 Homo sapiens cDNA clone 128434 5' similar to gb:X06764
DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION R10529
NID 9762485
KEYWORDS EST
SOURCE human clone-128434 library-Soares fetal liver spleen INFLS
vector-pT73D (Pharmacia) with a modified polylinker host-DH10B
(ampicillin resistant) primer-M13p1 Psite1= Pac I Psite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus; 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5',
AAGTGGAGAAATTAATTAAGATCTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 401)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,P.
The WashU-Merck EST Project
Unpublished (1995)

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 239
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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/clone="128434"

BASE COUNT 86 a 113 c 105 g 96 t 1 others
ORIGIN

Query Match 63.8%; Score 203; DB 40; Length 401;
Best Local Similarity 92.1%; Pred No. 0.00e+00;
Matches 293; Conservative 5; Mismatches 12; Indels 13; Gaps 13;

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QY 14 CTCAGGACACCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 73
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Db 254 tgggtctggggacagagatttactcttaccacacacagcagcagcagcagcagcagcagc 313
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QY 192 TGGGTCTGGG-ACAGACATTTACTCTT-CAGCAT-CAGTACACTGG-AGCTTGAAGATTTT- 246
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Db 374 ccaagtttggagatcaaa 391
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RESULT 6 H44798 399 bp mRNA EST 31-JUL-1995
LOCUS YP24a10.r1 Homo sapiens cDNA clone 188346 5' similar to gb:X06764
DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION H44798
NID 9920850
KEYWORDS EST.
SOURCE human clone-188346 library-Soares breast 3NBHst vector-pT73D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13p1 Rsite1=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCATCTGAGTGGAGCGCGCCCTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20 Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chcanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 399)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 289
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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Source /organism="Homo sapiens"
/clone="188346"

BASE COUNT 88 a 112 c 104 g 91 t 4 others
ORIGIN

Query Match 61.3%; Score 195; DB 69; Length 399;
Best Local Similarity 92.3%; Pred No. 0.00e+00;
Matches 250; Conservative 0; Mismatches 14; Indels 7; Gaps 7;

Db 70 acgcagctnccagcaccctctgttctcaggggaaagagccaccctctctctcagc 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7 AGGCAGTCTCCAGGACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 65
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 gccagtcagatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 GCCAGTCAGAGTGTAGGAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```









QY 136 CTATCATGGTGTATCCACAGGCGCCACTGGCATCCAGACAGGTTTCAGT 186

RESULT 13  
LOCUS H26475 385 bp mRNA EST 10-JUL-1995  
DEFINITION Y151905.r1 Homo sapiens cDNA clone 161816 5' similar to gb:M63438  
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);  
ACCESSION H26475  
NID 989598  
KEYWORDS EST  
SOURCE human clone-161816 library-Soares breast 3NHBst vector-p773D  
(Pharmacia) with a modified polylinker host-DHI08 (ampicillin  
resistant) primer-M13P1 PstI-EcoRI PstI-EcoRI Adult female  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],  
digested with Not I and ligated to Eco RI adaptors (Pharmacia),  
modified p773 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento  
Soares and M.Fatima Bernaldo

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo;  
1 (bases 1 to 385)  
REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 150  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source 1..385  
Location/Qualifiers  
/organism="Homo sapiens"  
/clone="161816"  
BASE COUNT 82 a 117 c 86 g 90 t 10 others  
ORIGIN

Query Match 43.4%, Score 138, DB 64, Length 385;  
Best Local Similarity 82.7%, Pred. No. 1,21e-224;  
Matches 220; Conservative 0; Mismatches 48; Indels 8; Gaps 6.

Db 73 acacagtcctccagccctctctttgtcccgaggagagacacccctctnagcagg 132  
QY 7 ACCGAGTCTCCAGGACCGCTGTGTTGTCTCCAGGGGAAGAGCCACCTCTCTGGGG 66  
Db 133 gccagtcacaaattcttctt---caagttcttagtctggtaccacagagccctnagcaggct 189  
QY 67 GCCAGTCAGAGTCTTAGGAGCAACTACTTAGGCTGTGTACGCAAAAACCTGGCAGGCT 126  
Db 190 nccaggtcctcctatgatatacatcaccagggccctctgggtccacagcagatttccac 249  
QY 127 CCGAGTCTCTATCATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 185  
Db 250 tggcagtggtgntctgagacagacttctccttccacatcagcagcctagagccctgaaaga 309  
QY 186 TGGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 242  
Db 310 ttttgaattattattatngtcagcag 335

QY 243 TTTTCAGTGTATTACT-GTCAGCAG 267

RESULT 14  
LOCUS R48043 421 bp mRNA EST 18-MAY-1995  
DEFINITION YJ56901.r1 Homo sapiens cDNA clone 153720 5' similar to gb:X06764  
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);  
ACCESSION R48043  
NID 9810069  
KEYWORDS EST  
SOURCE human clone-153720 library-Soares breast 2NHBst vector-p773D  
(Pharmacia) with a modified polylinker host-DHI08 (ampicillin  
resistant) primer-M13P1 PstI-EcoRI PstI-EcoRI Adult female  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],  
digested with Not I and ligated to Eco RI adaptors (Pharmacia),  
modified p773 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 230. Library constructed by Bento  
Soares and M.Fatima Bernaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo;  
1 (bases 1 to 421)  
REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 242  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source 1..421  
Location/Qualifiers  
/organism="Homo sapiens"  
/clone="153720"  
BASE COUNT 80 a 114 c 110 g 110 t 7 others  
ORIGIN

Query Match 43.1%, Score 137, DB 27, Length 421;  
Best Local Similarity 90.6%, Pred. No. 1.41e-222;  
Matches 174; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

Db 75 ctccagcagccctctcttctctccagggagggagccacccctctctctcacacagcagtc 134  
QY 14 CTCAGGACACCTGTGTTCTGTCAGAGGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 73  
Db 135 aagctctcagcagcagctacttagcctgggttcacagcagagagcctggccagcctccacagc 194  
QY 74 ACAGGTGTAGGAGCAACTTACTTAGCTCTGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 133  
Db 195 tccctcatctatgttgcataccacagggagggagggagggagggagggagggagggagggaggg 254  
QY 134 TCCTCATCTATGGTGTATCCAGCAGGG-CCACTGGCAT-CCACACAGGTT-CAGTGG-C 184  
Db 255 agtgggtctnng 266  
QY 190 AGTGGGTCTGGG 201

Search completed: Tue Feb 24 09:02:18 1998  
Job time : 291 secs.

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RESULT 15
LOCUS 151922 361 bp mRNA EST 18-MAY-1995
DEFINITION Y71B07.r1 Homo sapiens cDNA clone 154165 5' similar to
gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
ACCESSION R51922
NID g813824
KEYWORDS EST.
SOURCE human clone=154165 library=Soares breast 2NBHst vector=pf7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13P1 psite1=Not I psite2=Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
IGTACCAATCTGAGAGGAGGGGCGCCCTTTTCTTTTCTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified p7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 361)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, E.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 308
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
1..361
organism="Homo sapiens"
/cclone="154165"

BASE COUNT 75 a 108 c 91 g 83 t 4 others
ORIGIN

Query Match 41.5% Score 132: DB 28: Length 361:
Best Local Similarity 95.7%: Pred. No. 3,220-212:
Matches 228: Conservative 9: Mismatches 26: Indels 12: Gaps 11:

Db 91 ctccagcccccctctctctctctccgggggaagaagaatcacccctctctccgagggccactc 150
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Gy 14 ctccagcccccctctctctctctccgggggaagaagaatcacccctctctccgagggccactc 73
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 151 agagattt-gc-caacaacttagcctgattccagcagaagaacccctggcgccagctcccaag 207
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Gy 74 agagattttagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 132
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Db 208 cctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct 267
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Gy 133 ctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct 188
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Db 268 cctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct 327
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Gy 189 cagtggtt-ctctctctctctctctctctctctctctctctctctctctctctctctctctct 245
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 328 tucagctctattattctctctctctctctctctctctctctctctctctctctctctctctct 353
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Gy 246 tgcagctctattattctctctctctctctctctctctctctctctctctctctctctctctct 270
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```

21.



CC TELEPHONE: 415-326-2400  
CC TELEFAX: 415-326-2422  
CC INFORMATION FOR SEQ ID NO: 182:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 900 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: join(116..163, 351..550)  
SQ Sequence 900 BP: 220 A; 241 C; 201 G; 238 T; 0 other:  
  
Query Match 84.0%; Score 267; DB 7; Length 900;  
Best Local Similarity 98.2%; Pred. No. 1.32e-178;  
Matches 272; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
Db 375 ACCGAGTCTCCAGGACCTGCTGTTGCTCCAGGGGAAGGCGGCGCTCTCTCGAGG 434  
QY 7 ACCGAGTCTCCAGGACCTGCTGTTGCTCCAGGGGAAGGCGGCGCTCTCTCGAGG 66  
  
Db 435 GCCAGTCAGAGTGTAGCAGCAGTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 494  
QY 67 GCCAGTCAGAGTGTAGGAGCACTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
  
Db 495 CCCAGCTCTCTATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554  
QY 127 CCCAGCTCTCTATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
  
Db 555 GGCAGTGGGCTGGGACAGACTTCTCTCAGCAGCAGCTGAGGCGCTGGAAGATTTT 614  
QY 187 GGCAGTGGGCTGGGACAGACTTCTCTCAGCAGCAGCTGAGGCGCTGGAAGATTTT 246  
  
Db 615 GCAGTGTATTATGTCAGCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651  
QY 247 GCAGTGTATTATGTCAGCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 283

RESULT 2  
ID PCT-US93-12501-1 STANDARD; DNA: UNC; 325 BP.  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 1, Application PC/TUS9312501.  
CC Sequence 1, Application PC/TUS9312501  
CC GENERAL INFORMATION:  
CC APPLICANT: Chang, Tse Wen  
CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IgA MONOCLONAL ANTIBODIES AND  
CC TITLE OF INVENTION: RELATED PRODUCTS FOR ALLERGY TREATMENT  
CC NUMBER OF SEQUENCES: 10  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Tanox Biosystems, Inc.  
CC STREET: 10301 Stella Link Rd.  
CC CITY: Houston  
CC STATE: Texas  
CC COUNTRY: USA  
CC ZIP: 77025  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Hi Density Diskette  
CC COMPUTER: IBM PS/2  
CC OPERATING SYSTEM: DOS, Version 3.30  
CC SOFTWARE: Wordperfect 5.1  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PC1/US93/12501  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Mirabel, Eric P.  
CC REGISTRATION NUMBER: 31,211  
CC REFERENCE/DOCKET NUMBER: TXN92-3

CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 713-664-2288  
CC TELEFAX: 713-664-8914  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 325 nucleotides  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double stranded  
CC TOPOLOGY: Linear  
SQ Sequence 325 BP: 79 A; 93 C; 79 G; 74 T; 0 other:  
  
Query Match 82.4%; Score 262; DB 11; Length 325;  
Best Local Similarity 92.0%; Pred. No. 8.07e-175;  
Matches 287; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
  
Db 13 ACCGAGTCTCCAGGACCTGCTGTTGCTCCAGGGGAAGGCGGCGCTCTCTCGAGG 72  
QY 7 ACCGAGTCTCCAGGACCTGCTGTTGCTCCAGGGGAAGGCGGCGCTCTCTCGAGG 66  
  
Db 73 GCCAGTCAGAGTGTAGCAGCAGTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 132  
QY 57 GCCAGTCAGAGTGTAGGAGCACTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
  
Db 133 GGCAGTGGGCTGGGACAGACTTCTCTCAGCAGCAGCTGAGGCGCTGGAAGATTTT 192  
QY 127 GGCAGTGGGCTGGGACAGACTTCTCTCAGCAGCAGCTGAGGCGCTGGAAGATTTT 186  
  
Db 193 GGCAGTGGGCTGGGACAGACTTCTCTCAGCAGCAGCTGAGGCGCTGGAAGATTTT 252  
QY 187 GGCAGTGGGCTGGGACAGACTTCTCTCAGCAGCAGCTGAGGCGCTGGAAGATTTT 246  
  
Db 253 GCAGTGTATTATGTCAGCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312  
QY 247 GCAGTGTATTATGTCAGCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306  
  
Db 313 GTTGAATCAAA 324  
QY 307 TTGGAGATCAAA 318

RESULT 3  
ID PCT-US95-11235-2 STANDARD; DNA: UNC; 646 BP.  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 2, Application PC/TUS9511235.  
CC Sequence 2, Application PC/TUS9511235  
CC GENERAL INFORMATION:  
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNODOMAIN LIGHT  
CC CHAINS  
CC NUMBER OF SEQUENCES: 70  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: The Scripps Research Institute  
CC STREET: 10666 North Torrey Pines Road, TPC8  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/11235  
CC FILING DATE: 01-SEP-1995  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/300,386  
CC FILING DATE: 02-SEP-1994  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/174,674



CC FILLING DATE: 28-DEC-1993  
 CC PRIOR APPLICATION DATA: US 07/825,623  
 CC FILING DATE: 27-JAN-1992  
 CC PRIOR APPLICATION DATA: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC PRIOR APPLICATION DATA: US 08/012,566  
 CC FILING DATE: 02-FEB-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1 (P)  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 646 base pairs  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: cDNA  
 CC HYPOTHETICAL: NO  
 CC ANTI-SENSE: NO  
 CC Sequence 646 BP: 162 A; 187 C; 170 G; 127 T; 0 other;  
 CC  
 CC Query Match 81.4%; Score 259; DB 13; Length 646;  
 CC Best Local Similarity 93.1%; Pred No 1.50e-172;  
 CC Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;  
 CC  
 Db 1 GAGTTCACGAGTCTCCAGGACACCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60  
 QY 1 GAGTTCACGAGTCTCCAGGACACCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60  
 Db 61 TCGAGGGGCAATCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 QY 61 TCGAGGGGCAATCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 Db 121 CAGGCTCCAGGCTCCATCTATGATATGATATGATATGATATGATATGATATGATATG 180  
 QY 121 CAGGCTCCAGGCTCCATCTATGATATGATATGATATGATATGATATGATATGATATG 180  
 Db 181 TCCAGTGGGAGTGGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 QY 181 TCCAGTGGGAGTGGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 Db 241 GATTTTCAGTGTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 297  
 QY 241 GATTTTCAGTGTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 297  
 Db 298 ACCAAGGTGGAACTCAAA 315  
 QY 301 ACCAAGTGGAGATCAAA 318  
 CC  
 CC RESULT 4  
 CC ID US-08-300-386A-2 STANDARD: DNA; UNC; 646 BP.  
 CC AC XXXXX  
 CC DT 01-JAN-1990  
 CC DE Sequence 2, Application US/08300386A  
 CC Sequence 2, Application US/08300386A  
 CC Patent No. 5567948  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Barbas, Carlos F,III  
 CC APPLICANT: Burton, Dennis R  
 CC APPLICANT: Berner, Richard A  
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
 CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT  
 CC CHAINS  
 CC NUMBER OF SEQUENCES: 70  
 CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute  
 CC STREET: 10566 NO 56K7e88th Torrey Pines Road, IPC8  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/300,386A  
 CC FILING DATE: 02-SEP-1994  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/174,674  
 CC FILING DATE: 28-DEC-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/825,623  
 CC FILING DATE: 27-JAN-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/012,566  
 CC FILING DATE: 02-FEB-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 646 base pairs  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: cDNA  
 CC HYPOTHETICAL: NO  
 CC ANTI-SENSE: NO  
 CC Sequence 646 BP: 162 A; 187 C; 170 G; 127 T; 0 other;  
 CC  
 CC Query Match 81.4%; Score 259; DB 7; Length 646;  
 CC Best Local Similarity 93.1%; Pred No 1.50e-172;  
 CC Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;  
 CC  
 Db 1 GAGTTCACGAGTCTCCAGGACACCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60  
 QY 1 GAGTTCACGAGTCTCCAGGACACCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60  
 Db 61 TCGAGGGGCAATCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 QY 61 TCGAGGGGCAATCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 Db 121 CAGGCTCCAGGCTCCATCTATGATATGATATGATATGATATGATATGATATGATATGATATG 180  
 QY 121 CAGGCTCCAGGCTCCATCTATGATATGATATGATATGATATGATATGATATGATATGATATG 180  
 Db 181 TCCAGTGGGAGTGGGCTGGGAG 240  
 QY 181 TCCAGTGGGAGTGGGCTGGGAG 240  
 Db 241 GATTTTCAGTGTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 297  
 QY 241 GATTTTCAGTGTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 297  
 Db 298 ACCAAGGTGGAACTCAAA 315  
 QY 301 ACCAAGTGGAGATCAAA 318

RESULT 5  
ID PCT-US94-01258-2 STANDARD; DNA: UNC; 646 BP  
AC xxxxxx  
DE 01-JAN-1900  
DT Sequence 2, Application PCT/US9401258.  
CC Sequence 2, Application PCT/US9401258  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES  
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT  
CC CHAINS  
CC NUMBER OF SEQUENCES: 61  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: Patent In Release #1 0, Version #1 25 (EPO)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US94/01258  
CC FILING DATE: 02-FEB-1994  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/012,566  
CC FILING DATE: 03-FEB-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/174,674  
CC FILING DATE: 28-DEC-1993  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 646 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;  
  
Query Match 81.4%; Score 259; DB 12; Length 646;  
Best Local Similarity 93.1%; Pred. No. 1,50e-172;  
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1,  
  
Db 1 GAGCTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCC 60  
QY 1 GAGCTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCC 60  
Db 61 TCCAGGCGCCAGTACAGTGTAGCAGGGGACTTACCTAGCCTGTACACGACGAAACCTGGC 120  
QY 61 TCGGGGGCCAGTACAGTGTAGGAGCAACTTACCTAGCCTGTACACGACGAAACCTGGC 120  
Db 121 CAGGCTCCAGGCTCCTCATCTATGATGATCCAGGCGCCACTGGCATCCAGACAGG 180  
QY 121 CAGGCTCCAGGCTCCTCATCTATGATGATCCAGGCGCCACTGGCATCCAGACAGG 180  
Db 181 TCCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAA 240  
QY 181 TCCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAA 240  
Db 241 GATTTTGCAGTGTACTGTCTCAGCAGTATGGTGTACCCCTGG- --TTGGCCCAAGGG 297  
QY 241 GATTTTGCAGTGTACTGTCTCAGCAGTATGGTGTACCCCTGG- --TTGGCCCAAGGG 297  
Db 298 ACCAAGGTGGAACCTCAA 315  
QY 301 ACCAAGTTGGAGATCAA 318  
  
RESULT 6  
ID US-08-276-852-152 STANDARD; DNA: UNC; 729 BP.  
AC xxxxxx  
DE 01-JAN-1900  
DT Sequence 152, Application US/08276852  
CC Sequence 152, Application US/08276852

CC Patent No. 5652138  
CC GENERAL INFORMATION:  
CC APPLICANT: Burton, Dennis R  
CC APPLICANT: Barbas, Carlos F  
CC APPLICANT: Lerner, Richard A  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: The Scripps Research Institute, Office of  
CC ADDRESSEE: Patent Counsel  
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/276,852  
CC FILING DATE: 18-JUL-1994  
CC CLASSIFICATION: 514  
CC PRTOP APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/178,302  
CC FILING DATE: 30-SEP-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/954,148  
CC FILING DATE: 30-SEP-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: SCPI452P  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-554-2937  
CC TELEFAX: 619-554-6312  
CC INFORMATION FOR SEQ ID NO: 152:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 729 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 9..715  
SQ Sequence 729 BP; 173 A; 238 C; 192 G; 156 T; 0 other;  
  
Query Match 69.5%; Score 221; DB 7; Length 729;  
Best Local Similarity 85.1%; Pred. No. 7.20e-144;  
Matches 268; Conservative 0; Mismatches 47; Indels 0; Gaps 0.  
  
Db 78 CTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCTGT 137  
QY 4 CTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCTGT 63  
Db 138 AGGTCCAGTCCAGCAATTCGCGAGCGCGGGGTAGCTGTGTTAGTACAGCAAACTTGGGTAG 197  
QY 64 GGGGCGAGTCCAGAGTGTAGGAGCACTTACTTAGCTGTGTAGTACAGCAAAACTTGGGTAG 123  
Db 198 GCTCCAAAGGCTGCTATACATATGTTTCCAAATAGGGGCTCTGGCATCTCCAGACAGTTTC 257  
QY 124 GTCCTCCAGGCTCTCTCATCTATGTTGTTATCCAGGAGGCGCACTGGCATCCAGACAGTTTC 193  
Db 258 ACCGCGAGTGGGTCTGCGACAGACATTCACATCTCAAAATACAAAGTGGAGGCTTGAAGAC 317  
QY 184 AGTGGCAGTGGGTCTGCGACAGACATTCACATCTCAAAATACAAAGTGGAGGCTTGAAGAT 243  
Db 318 TTTGCACTGTACTACTGTACAGTCTTATGGTGGCTTCTGCTACACTTTTGGCAGGCGACCC 277



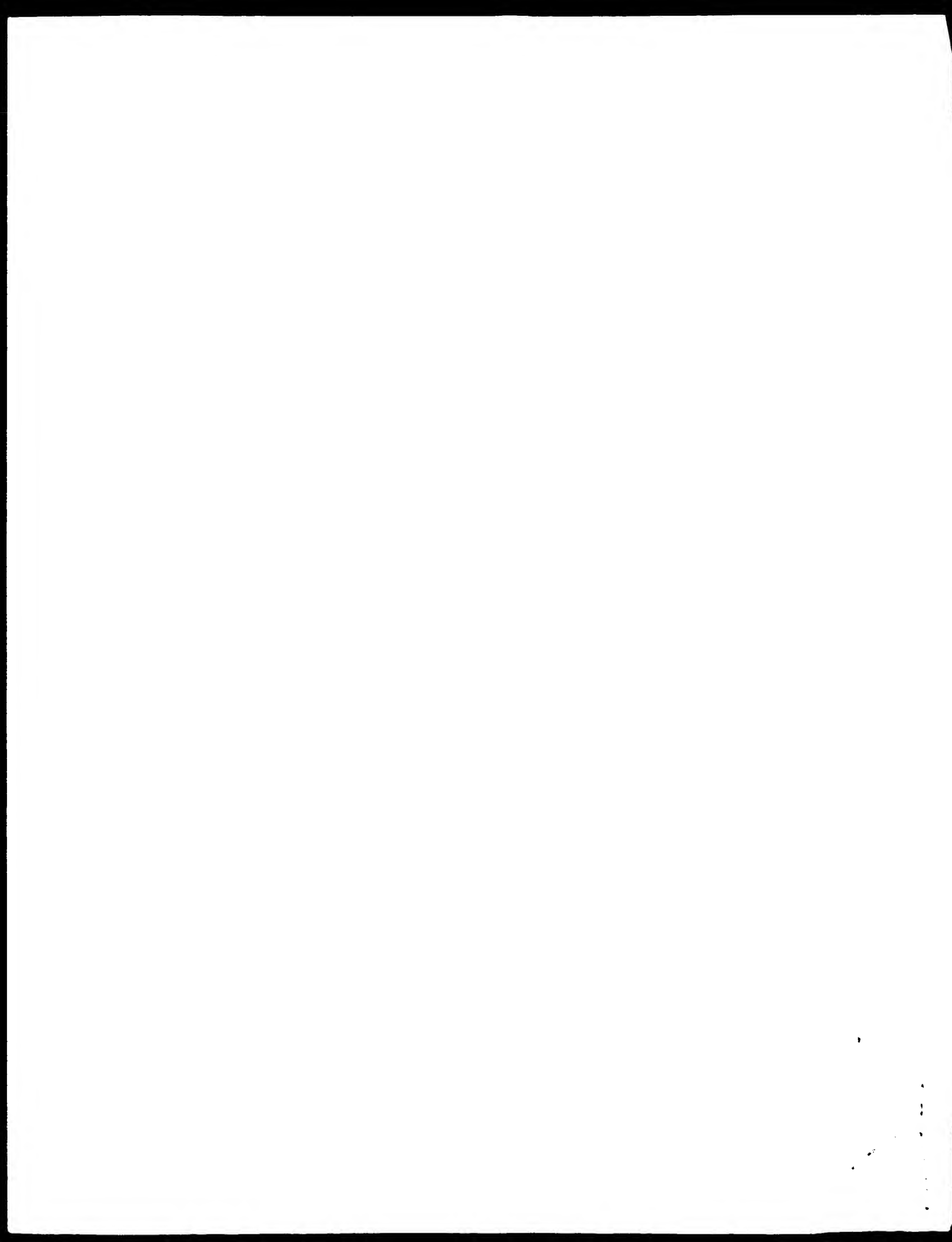


[illegible]

CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC OPERATING SYSTEM: IBM PC Compatible  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276.852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCF1452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 170:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 13254 base pairs  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: double  
 CC TOPOLOGY: circular  
 CC MOLECULE TYPE: DNA (genomic)  
 CC Sequence 13254 BP: 3238 A: 3251 C: 3559 G: 3206 T: 0 other:  
 CC  
 CC Query Match 69.5%; Score 221; DB 7; Length 13254.  
 CC Best Local Similarity 85.1%; Pred. No. 7.20e-144;  
 CC Matches 268; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
 CC  
 Db 335 TTTCCTCTCCAGTTGGTCCCTGCGCAAAAGTGTACGAGGAGGACCATAGACCTGACA 394  
 Cp 318 TTGTATCTCCAACTGGTCCCTGCGCAAAAGTGTACGAGGAGGACCATAGACCTGACA 259  
 Db 395 GTAGTACAGTCAAAAGTCTTCAGGCTCCACTCTGCTGAGAGTGAAGTGTGCCC 454  
 Cp 258 GTAATACAGTCAAAAGTCTTCAGGCTCCACTCTGCTGAGAGTGAAGTGTGCCC 199  
 Db 455 AGACCACTGCGGCTGACCTCTGTGAGTGCACAGGCGCCCTATTGGAACACCATGAT 514  
 Cp 198 AGACCACTGCGGCTGACCTCTGTGAGTGCACAGGCGCCCTATTGGAACACCATGAT 139  
 Db 515 GACCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 574  
 Cp 138 GAGGAGCTGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 79  
 Db 575 GCTGTACTGGAGCTACAGGAGAGGCTGCTTTCCTCTGGAGAGAGAGGCTGCTTTC 634  
 Cp 78 ACTCTACTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 19  
 Db 635 TGGAGACTGCTGAG 649  
 Cp 18 TGGAGACTGCTGAG 4  
 CC  
 RESULT 14  
 ID US-08-053-131-178 STANDARD; DNA: UNC; 812 BP.  
 AC xxxxxx  
 DT 01-JAN-1900  
 DE Sequence 178, Application US/08053131.  
 CC Sequence 178, Application US/08053131  
 CC Patent No. 5661016  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Lonberg, Nils  
 CC APPLICANT: Kay, Robert M.  
 CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
 CC TITLE OF INVENTION: Producing Heterologous Antibodies

CC NUMBER OF SEQUENCES: 197  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Townsend Kourile and Crew  
 CC STREET: One Market Plaza, Stewart Tower, Suite 200  
 CC CITY: San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94105  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC OPERATING SYSTEM: IBM PC Compatible  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/053,131  
 CC FILING DATE: 26-APR-1993  
 CC CLASSIFICATION: 800  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/990,860  
 CC FILING DATE: 16-DEC-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/810,279  
 CC FILING DATE: 17-DEC-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/853,408  
 CC FILING DATE: 18-MAR-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Smith, William M.  
 CC REGISTRATION NUMBER: 30,223  
 CC REFERENCE/DOCKET NUMBER: 14643-9-3  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415-326-2400  
 CC TELEFAX: 415-326-2422  
 CC INFORMATION FOR SEQ ID NO: 178:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 812 base pairs  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: DNA (genomic)  
 CC FEATURE:  
 CC NAME/KEY: CDS  
 CC LOCATION: join(190, 246, 418, 714)  
 CC Sequence 812 BP: 201 A: 205 C: 187 G: 199 T: 0 other:  
 CC  
 CC Query Match 67.9%; Score 216; DB 7; Length 812;  
 CC Best Local Similarity 91.7%; Pred. No. 4.17e-140;  
 CC Matches 234; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
 CC  
 Db 442 ACACAGTCTCCAGGACCCCTGCTTTGTCTCCAGGGGAAAGAGCCACCTCTCTGCGG 501  
 QY 7 AGCGAGTCTCCAGGACCCCTGCTTTGTCTCCAGGGGAAAGAGCCACCTCTCTGCGG 66  
 Db 502 GCGAGTCTAGAGTGTAGCAGC---TACTTAGCTGGTATCCACAGAGAACTGCTAGGCT 558  
 QY 67 GCGAGTCTAGAGTGTAGCAGC---TACTTAGCTGGTATCCACAGAGAACTGCTAGGCT 126  
 Db 559 CCCAGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618  
 QY 127 CCCAGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186  
 Db 619 GCGAGTCTGAGGACAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 478  
 QY 187 GCGAGTCTGAGGACAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246  
 Db 679 GCGAGTCTGAGGACAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 715  
 QY 247 GCGAGTCTGAGGACAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 283  
 CC  
 RESULT 15  
 ID US-08-053-131-180 STANDARD; DNA: UNC; 900 BP.  
 AC xxxxxx







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WIRETEL

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MPSrch\_nnn n a - n a database search using Smith-Waterman algorithm

Run on: Tue Feb 24 07:55:39 1998 MasPar time 48.40 seconds  
758,215 Million cell updates/sec

Tabular output not generated

Title: >US-08-844-215-17  
Description: (1-318) from US08844215.seq  
Perfect Score: 318  
N.A. sequence: 1 CAGCTCAGCGAGTGTCCAGG  
Comp: CUCAGTCCGCTACAGTTC

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 159651 seqs, 57699962 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq30  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.015; Variance 4.892; scale 1.638

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

SUMMARIES

Result No	Score	Query Match	Length	ID	Description	Pred. No.
1	278	87	4	Q49155	F105 rearranged varia	1 34e-169
2	276	86	9	P105V4-F105V4	P105V4-F105V4	1 34e-169
3	270	84	9	772922	Immunoglobulin epsilon	4 62e-164
4	267	84	0	772922	Immunoglobulin epsilon	5 61e-162
5	267	84	0	772922	Immunoglobulin epsilon	5 61e-162
6	267	84	0	772922	Immunoglobulin epsilon	5 61e-162
7	264	83	0	Q49155	Human DNA fragment vk	5 51e-162
8	262	82	4	Q49155	Human DNA fragment vk	5 51e-162
9	262	82	4	Q49155	Human DNA fragment vk	5 51e-162
10	261	82	1	Q49155	Human DNA fragment vk	5 51e-162
11	261	82	1	Q49155	Human DNA fragment vk	5 51e-162
12	259	81	4	Q49155	Human DNA fragment vk	5 51e-162
13	258	81	4	Q49155	Human DNA fragment vk	5 51e-162
14	257	80	8	Q49155	Human DNA fragment vk	5 51e-162
15	252	79	2	Q49155	Human DNA fragment vk	5 51e-162

16	249	78	3	642	25	T44920	Vaccinating cell surface	1 52e-149
17	239	75	2	1011	1	N81592	Anti-P. aeruginosa s	1 21e-142
18	239	75	2	1011	1	N81592	Anti-P. aeruginosa s	1 21e-142
19	229	72	0	924	10	Q11972	Sequence coding human	9 42e-136
20	224	70	4	324	16	Q42644	PM2A fragment, mouse	2 61e-132
21	221	69	5	729	24	T40912	DNA encoding modified	2 61e-130
22	221	69	5	729	24	T40912	DNA encoding modified	2 61e-130
23	216	67	9	812	27	T37180	Nucleotide sequence of	9 27e-127
24	216	67	9	812	27	T37180	Nucleotide sequence of	9 27e-127
25	216	67	9	812	27	T37180	Nucleotide sequence of	9 27e-127
26	212	65	7	900	12	Q78953	Human DNA fragment vk	4 63e-124
27	212	65	7	900	12	Q78953	Human DNA fragment vk	4 63e-124
28	212	65	7	900	12	Q78953	Human DNA fragment vk	4 63e-124
29	209	65	7	1204	2	Q11972	IgG light chain varia	5 31e-122
30	209	65	7	1204	2	Q11972	IgG light chain varia	5 31e-122
31	164	51	6	416	31	T19345	cDNA encoding kappa 1	2 97e-91
32	150	47	2	439	33	T73443	Human immunoglobulin	9 25e-82
33	150	47	2	439	33	T73443	Human immunoglobulin	9 25e-82
34	148	46	5	324	2	N81592	Anti-pseudomonas aer	2 69e-80
35	148	46	5	324	2	N81592	Anti-pseudomonas aer	2 69e-80
36	148	46	5	324	2	N81592	Anti-pseudomonas aer	2 69e-80
37	147	46	2	341	28	T60117	Coding sequence for 1	2 93e-80
38	146	45	9	388	33	T73441	Human immunoglobulin	4 69e-79
39	144	45	3	645	13	Q67896	cDNA contg. an ORF fo	1 05e-77
40	143	45	0	324	33	T60119	Anti-TGF beta-2 scf	4 98e-77
41	141	44	3	341	28	T60119	Coding sequence for 1	1 11e-75
42	141	44	3	341	28	T60119	Coding sequence for 1	1 11e-75
43	141	44	3	341	28	T60119	Coding sequence for 1	1 11e-75
44	141	44	3	341	28	T60119	Coding sequence for 1	1 11e-75
45	140	44	0	552	33	T90023	DNA encoding light ch	5 26e-75

ALIGNMENTS

RESULT 1  
ID Q49155 standard: cDNA; 387 BP.  
AC Q49155:  
DI 01-NOV-1993 (first entry)  
DE F105 rearranged variable region light chain.  
KW Monoclonal antibody, MAb, envelope, glycoprotein, gp120; HIV; AIDS;  
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;  
KW Chain; epitope; immune deficiency; SS  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT sig\_peptide 1 57  
FT /\*tag= a  
FT mat\_peptide 58...387  
FT /\*tag= b  
PN W09312232-A.  
PD 24-JUN-1993.  
PF 10-DEC-1992; W10929.  
PP 10-DEC-1991; US-804552.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (NEWB) NEW ENGLAND DEACONNESS HOSPITAL CORP.  
PI Haseltine WA, Mardisco WA, Posner MR, Sodroski JG;  
DR WPI: 93-214174/26.  
DP P-PSDB: P41286.  
DI DNA segments encoding monoclonal antibody - which binds to gp120  
PI and neutralises HIV, for treating AIDS, and for diagnosing and  
PI monitoring HIV infection  
ES Claim 1, Page 79, 109pp; English  
CC mRNA from the known hybridoma F105 was converted to cDNA and this  
CC subjected to PCR amplification using primers derived from appropriate  
CC parts of the heavy or light chains and having restriction sites to  
CC permit cloning. The extension products were isolated and sequenced.  
CC The recombinant human monoclonal antibody (MAb) binds to a  
CC discontinuous epitope on the HIV gp120 envelope glycoprotein. Blocks  
CC the binding of gp120 to the CD4 receptor, and neutralises a broad  
CC range of HIV isolates. The MAb may be used to treat immune  
CC deficiency, esp at doses of 0.1-10 mg/kg.  
SQ Sequence 387 bp; 88 A; 111 C; 101 G; 87 T;  
Query Match 87.4%; Score 278, DB 7; Length 387;

Best Local Similarity 94.6%; Pred. No. 1.34e-169; Matches 295; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db 73 acgagctccagcagccactcttctcagcaggggaaagagccaccctctcctcagc 132  
 QY 7 ACCGAGTCTCCAGGACCCCTGCTCTGCTCCAGGGGAAGAGCCACCTCTCTCGGG 66

Db 133 gccadtcagagtggttagcagcaggtacttagcctcgtggtaccagcagaaacccctgcccagct 192  
 QY 67 GCCAGTCCAGAGTGTAGGAGCAACTACTTAGCTGTGGTACGAGCAAAACCTGGCCAGGCT 126

Db 193 cccagctcctcctatcgtgctcagcagcagggccactggccatccacagaggttcagt 252  
 QY 127 CCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGGAAGAGCCACCTCTCTCGGG 132

Db 253 gccagtggtgctggcagcagctcactcctcagcagcaggtggagcctgaagatttt 312  
 QY 187 GCACTGCTGCTGGCAGCAAGCTTACTCTCAGCATCAGCAGACTGGAAGCTGAAGATT 246

Db 313 gcagtgattactgcagcaatagataactcctgcttctgacttttggccaggggacacag 372  
 QY 247 GCAGTGTATTACTGTCAGCAGTATGATGATGATGATGATGATGATGATGATGAT 306

Db 373 ctggagagatcaaa 384  
 QY 307 TTGGAGATCAAA 318

RESULT 2  
 ID Q42707 standard; DNA; 390 BP.  
 AC Q42707;  
 DT 01-NOV-1993 (first entry)  
 DE F105VK-F105JK.  
 KW Monoclonal antibody; MAbs; envelope; glycoprotein; gp120; HIV; AIDS;  
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;  
 KW chain; epitope; immune deficiency; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /\*tag= a  
 FT mat\_protein 61..390  
 FT /\*tag= b  
 FT misc\_RNA 1..351  
 FT /\*tag= c  
 FT label= F105VK 352..390  
 FT misc\_PNA  
 FT /\*tag= d  
 FT label= F105JK 130..165  
 FT misc\_PNA  
 FT /\*tag= e  
 FT label= CDR1 211..231  
 FT misc\_PNA  
 FT /\*tag= f  
 FT label= CDR2 328..354  
 FT misc\_PNA  
 FT /\*tag= g  
 FT label= CDR3  
 PN W09312232-A.  
 PD 24-JUN-1993  
 PE 10-DEC-1992; 010928  
 PR 10-DEC-1991; 010928  
 PA (DAND) DANA FARRER CANCER INST INC.  
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.  
 PI Haseltine WA, Marasco WA, Posner MP, Sodroski TG;  
 DR WPI: 93-214174/26.  
 DP P-PSDB: P38672.  
 PI DNA segments encoding monoclonal antibody - which binds to gp120  
 PI and neutralises HIV, for treating AIDS, and for diagnosing and  
 PI monitoring HIV infection  
 PS Disclosure, Page 73-74; 10pp; English  
 CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from  
 CC other F105 VK sequences given elsewhere in the specification) was  
 CC compared with germline gene Humv325 (Q42706), showing 97.7%

CC similarity. By nucleotide sequence analysis, F105 appears to  
 CC be derived from a member of the Vx III subgroup gene family.  
 SQ Sequence 390 BP, 86 A, 115 C, 102 G, 87 T,  
 Query Match 86.8%; Score 276; DB 7; Length 390;  
 Best Local Similarity 96.2%; Pred. No. 3.24e-168;  
 Matches 303; Conservative 0; Mismatches 9; Indels 3; Gaps 2;

Db 73 acgagctccagcagccactcttctcagcaggggaaagagccaccctctcctcagc 132  
 QY 7 ACCGAGTCTCCAGGACCCCTGCTCTGCTCCAGGGGAAGAGCCACCTCTCTCGGG 66

Db 133 gccadtcagagtggttagcagcaggtacttagcctcgtggtaccagcagaaacccctgcccagct 192  
 QY 67 GCCAGTCCAGAGTGTAGGAGCAACTACTTAGCTGTGGTACGAGCAAAACCTGGCCAGGCT 126

Db 193 cccagctcctcctatcgtgctcagcagcagggccactggccatccacagaggttcagt 252  
 QY 127 CCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGGAAGAGCCACCTCTCTCGGG 132

Db 253 gccagtggtgctggcagcagctcactcctcagcagcaggtggagcctgaagatttt 312  
 QY 187 GCACTGCTGCTGGCAGCAAGCTTACTCTCAGCATCAGCAGACTGGAAGCTGAAGATT 246

Db 313 gcagtgattactgcagcaatagataactcctgcttctgacttttggccaggggacacag 372  
 QY 247 GCAGTGTATTACTGTCAGCAGTATGATGATGATGATGATGATGATGATGATGAT 303

373 aagctggagatcaaa 387  
 304 AAGTTGGAGATCAAA 318

RESULT 3  
 ID T79922 standard; DNA; 372 BP.  
 AC T79922;  
 DT 09-OCT-1997 (first entry)  
 DE Immunoglobulin r101-2 light chain variable region coding sequence.  
 KW Immunoglobulin; variable region; heavy chain; thyrotropin receptor;  
 KW thyroid stimulating activity; light chain; Basedow's disease; antibody;  
 KW peripheral blood lymphocyte; ss  
 OS Homo sapiens.  
 PN J09140386-A.  
 PD 03-JUN-1997.  
 PE 22-NOV-1995; 328235.  
 PR 22-NOV-1995; JP-328235.  
 PA (EIKE) EIKEN KAGAKU KK.  
 DR WPI: 97-344899/32.  
 DE P-PSDB: W24539.  
 PT Antibody containing immunoglobulin heavy chain mutation - with  
 PT thyroid function stimulating activity  
 PS Claim 4; Page 12; 18pp; Japanese.  
 CC T79919-T79922 represent the immunoglobulin heavy and light chain variable  
 CC regions isolated from peripheral blood lymphocyte strains. These  
 CC sequences were isolated from the BeB7 and 101-2 strains of peripheral  
 CC blood lymphocytes of a Basedow's disease patient. These sequences are  
 CC replaced, deleted or inserted into an antibody, to create the antibodies  
 CC of the invention. The antibodies of the invention have thyroid function  
 CC stimulating activity, and act by combining with thyrotropin receptor. The  
 CC antibody can be used in a method to detect autoantibodies which have  
 CC thyroid function stimulating activity.  
 SQ Sequence 372 BP; 81 A; 115 C; 95 G; 81 T;  
 Query Match 84.9%; Score 270; DB 32; Length 372;  
 Best Local Similarity 95.0%; Pred. No. 4.62e-164;  
 Matches 285; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 73 acgagctccagcagccactcttctcagcaggggaaagagccaccctctcctcagc 132  
 QY 7 ACCGAGTCTCCAGGACCCCTGCTCTGCTCCAGGGGAAGAGCCACCTCTCTCGGG 66

Db 133 gccadtcagagtggttagcagcaggtacttagcctcgtggtaccagcagaaacccctgcccagct 192



DB 615 gcagtgattactgcagcagatgtagctcaccctc 651  
 AC Q44224:  
 DT 10-NOV-1993 (first entry)  
 DE Human DNA fragment vk65.8 containing V-kappa gene segment.  
 KW Immunoglobulin: light chain variable region; minilocus;  
 KW isotype switching; unrearranged functional V $\kappa$  gene segment;  
 KW human light chain transgene; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT misc\_signal 53..60  
 FT /\*tag= a  
 FT /note= "splicing and recombination signal ?"  
 FT exon 116..164  
 FT /\*tag= b  
 FT /number= 1  
 FT /note= "nucleotides 116-118 represent the  
 initiation codon, i.e. the start of the ORF;  
 the precise start point of the exon is not  
 indicated"  
 FT intron 165..351  
 FT /\*tag= c  
 FT exon 352..650  
 FT /\*tag= d  
 FT /note= "ORF not terminated by a stop codon"  
 FT misc\_recomb 653..680  
 FT /\*tag= e  
 FT /note= "splicing and recombination signal sequence"  
 PN WO931227-A.  
 PD 24-JUN-1993.  
 PR 17-DEC-1992; U10983.  
 PR 17-DEC-1991; US-810279.  
 PR 18-MAR-1992; US-853408.  
 PR 23-JUN-1992; US-904068.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N;  
 DR WPI: 93-214159/26.  
 DR P-PSDB; R38650.  
 PT Transgenic non-human animals contg. immunoglobulin heavy chain  
 PT trans gene - used to produce useful antibodies by isotype  
 PT switching  
 PS Example 21, Fig 43, 196pp, English.  
 CC The V-kappa specific oligonucleotide Q50327 was used to probe a  
 CC human placental genomic DNA library cloned into lambdaEMBL3/SP6/T7.  
 CC DNA fragments containing V-kappa segments from positive phage  
 CC clones were subcloned into plasmid vectors. Variable gene segments  
 CC from the resulting clones were sequenced and functional clones were  
 CC selected on the basis of open reading frames, intact donor and  
 CC acceptor splice sites and intact recombination sequences. The  
 CC sequences obtained from four different plasmid clones were  
 CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q4425,  
 CC respectively).  
 SQ Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;

Query Match 84.0%; Score 267; PR 7; Length 900;  
 Best Local Similarity 98.2%; Pred. No. 5; Size-162;  
 Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

DB 375 acgcagctccagagaccctgttcttctccagggaaagagaccctctctcagag 434  
 QY 7 ACAGTCTTCAGGACACCTGTCTTGTCTCCAGGGGAAAGAGCCACCTCTCTCGG 56  
 DB 435 gccactcagagtgtagcagcagctacttagcctgggtaccagcagaacacgtgccaggt 494  
 QY 67 GGCACCTACAGCTGTAGACGCAATATTTATGCTGTGTATACGAAAAATGACCAAG 126  
 DB 495 tccagctctcactatgtatgcacagcagggcagcagctagcaccagcagaggttcagt 554

QY 127 CCCAGGCTCTCTATCTATCTGTGTATCTCCAGACAGGAGGACATGCTATCTCTGATCT 186  
 DB 555 ggcagtgagggtctgggacacagctcactctcaccatcagagagctgagagcttatt 614  
 QY 187 GCCAGTGGGTCTGGGACAGACITCACTCTCACTCCAGCAGACACTGGAGCTGCAACATTT 246  
 DB 615 gcagtgattactgcagcagatgtagctcaccctc 651  
 QY 247 GCAGTGTATTACTGTCTCAGCAGTATGTTAGTCTCACCTC 283

## RESULT 7

ID T33664 standard: cDNA: 402 BP.

AC T33664:  
 DT 10-JUN-1997 (revised)  
 DT 14-MAY-1997 (first entry)  
 DE Anti-lung tumour antigen monoclonal antibody light chain cDNA.  
 KW Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;  
 KW Epstein-Barr virus; TB945; human; B cell; screen; antigen;  
 KW carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;  
 KW cell; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..402  
 FT /\*tag= a  
 PN WO9628473-A1.  
 PD 19-SEP-1996.  
 PR 18-MAR-1996; U03661.  
 PR 16-MAR-1995; US-405034.  
 PA (MEDE/) MEDENICA R D.  
 PI Mukerjee S;  
 DR WPI: 96-433764/43.  
 DR P-PSDB; W11155.  
 PT Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by  
 PT Epstein-Barr virus transformation of human lung cancer patient  
 PT B-cells, useful in conjunction with other agents for lysis of  
 PT tumours

PS Claim 12, Pages 24-25, 46pp, English

CC The present sequence encodes the light chain from the monoclonal  
 CC antibody (MAB) TB2A36C3, which has high specificity against lung  
 CC tumour antigens and is produced by an Epstein-Barr virus (EBV)  
 CC transformed TB945 human B cell line. The MAB can be used to screen  
 CC serum or tissue samples for a carcinoma associated antigen, lyse  
 CC tumours in anti-tumour therapy (optionally with other agents) and  
 CC activate immune competent CD4 or CD8 cells in a patient's blood  
 CC system.  
 CC Tumour draining lymph nodes obtained from a non-SCLC (small cell  
 CC lung cancer) patient were cut into fine pieces and mashed. Pure B  
 CC cells, isolated using CD19 coated immunomagnetic beads, were  
 CC immortalised by EBV transformation, and plated and assayed for  
 CC activity. Clones which showed positive reactivity with autologous  
 CC tumour cells from the patient and the SCLC cell line NCIH69, were  
 CC subjected to limiting dilution to prepare the MAB.  
 CC (Revised entry submitted to correct cross-reference to the  
 CC corresponding protein record (W11155)).  
 SQ Sequence 402 BP; 89 A; 117 C; 103 G; 93 T;

Query Match 83.0%; Score 264; PR 28; Length 402;

Best Local Similarity 94.3%; Pred. No. 6; Size-160;

Matches 297; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

DB 73 agcagctctcaggtacagctcagcttcttctccagggaaagagaccctctctcagag 130  
 QY 7 ACCAGCTCTCCAGGACCTCTGTCTTGTCTCCAGGGGAAAGAGACCTCTCTCTCGG 56  
 DB 133 gccagtcagaggttttagcagagaagctcttagctggtaccagcagaacacgtgagagct 192  
 QY 67 GCCAGTCAGAGTGTITTAGGAGCAACTACTTAGCTCTGTTACAGAAAAATCTGGCAGGCT 126  
 DB 193 cccagcctctctctctatgttctatccacccaggggtctatgggtatccagagagaggt 262  
 QY 127 CCCAGGCTCTCTATCTATCTGTGTATCTCCAGACAGGAGGACATGCTATCTCTGATCT 186



QY 127 CCAGGCTCTCTATCTATGTTATGCTATCCAGCAGGGCCACTGGCATCCACAGACAGGTTTCAGT 186  
 Db 253 ggcagtggtgtcgtggagacagactcactctccaccatccagcagagtgagcctggaagatttt 312  
 QY 187 GGCAGTGGGTCTGGGACACAGCTCTACTCTCACATCCACAGACACTGGAGCTTGAAGATTTT 246  
 Db 313 gcaagtattactgtcagcaaatatgataactcctgtttgtctacactttttggccaggggacc 372  
 QY 247 GCAGTGTATTACTGTCCAGCAGTATGTTAGTCTCACCCTCGG---ACTTTTGGCCAGGGGACC 303  
 Db 373 aagctggagatcaaa 387  
 QY 304 AAGTTGGAGATCAAA 318

RESULT 10  
 ID Q92546 standard; DNA: 4591 BP.  
 AC Q92546:  
 DT 11-MAR-1996 (first entry)  
 DE pComb3 expression vector.  
 KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;  
 KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;  
 KW Bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120;  
 KW Combinatorial Fab library; cassette; fd/cp3; lacZ promoter/operator;  
 KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;  
 KW MT4; pMT4-3; antibody; ss; cyclic  
 OS Synthetic.  
 PN WO9511317-A1.  
 PD 27-APR-1995.  
 PF 19-OCT-1994; U11907.  
 PR 19-OCT-1993; US-139409.  
 PR 26-APR-1994; US-233619.  
 PR 19-SEP-1994; US-308841.  
 PA (SCRI) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI: 95-170235/22.  
 PT Synthetic human neutralising monoclonal antibodies to human  
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of  
 PT HIV-induced disease  
 PS Example 1; Page 185-188; 249pp; English.  
 CC This sequence represents the pComb3 phagemid expression vector. This  
 CC vector has been designed to allow for anchoring of expressed proteins on  
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes  
 CC the 406 residue minor phage coat protein, cpIII (cp3), which is expressed  
 CC prior to extrusion in the phage assembly process on a bacterial membrane  
 CC and accumulates on the inner membrane facing into the periplasm of E.  
 CC coli. This plasmid was used within the scope of the invention to express  
 CC various mutagenised human Fab's which comprise heavy and light variable  
 CC regions which bind to HIV gp120. pComb3 allows for both surface display  
 CC and soluble forms of the Fab's. The vector was designed for the cloning  
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having  
 CC two cassettes to express one fusion protein, fd/cp3, and one soluble  
 CC protein, the light chain. The finished vector comprises, operatively  
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator  
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a  
 CC PelB leader, a spacer region, a cloning region bordered by 5' XhoI and  
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding  
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site  
 CC between the two cassettes, and a second lacZ promoter/operator sequence,  
 CC followed by an expression control RBS, a PelB leader, a spacer region, a  
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,  
 CC followed by expression control stop sequences and a second NotI  
 CC restriction site. The pComb3 expression vector forms the basic construct  
 CC of the MT4 Fab display phagemid expression vector, pMT4-3 (see also  
 CC Q92540), used in the invention for the production of synthetic human Fab  
 CC antibodies against gp120 of HIV.  
 SQ Sequence 463: BP 1170 A 1171 C 1232 G 1118 T

Query Match 82.1%; Score 261; DB 16; Length 4691;  
 Best Local Similarity 93.4%; Pred. No. 7,780-158;  
 Matches 297; Conservative 0; Mismatches 18; Indels 3; Gaps 1.

Db 26N7 ggcagtggtgtcgtggagacagactcactctccaccatccagcagagtgagcctggaagatttt 2746

QY 1 CAGCTACGCGAGTCTCCAGGTCACCGCTGTCTTTGTCTGTCTAGGGGAAAAGACACCCCTCTCC 50  
 Db 2737 tccagggccactccagctgttagcagggcctacttagcctggtaccagcagagaacctgac 2796  
 QY 61 TCGGGGGCCAGCTCAGAGTGTGTAGGAGCAACTATTTAGCTTGGTAGGCAAAAACCTGGG 120  
 Db 2797 cgggtctccaggtctccatctatgttggtacatccagcaggggcccactggcatcccaacac 2856  
 QY 121 CAGGCTCCAGGCTCCCTCATCTATGCTATGCTAGTAGGAGGCTACTGGCATCCACAGACAG 180  
 Db 2857 ttcagtgccagtggtcttgagacagacttcactctccaccatccagcagagactggagcctgaa 2916  
 QY 181 TTCAGTGGCAGTGGGTCTGGGACACAGCTTCACCTCATTACATACACACACACTGSSAGGCTGAA 240  
 Db 2917 gattttgcagtgctactactctacacatgatgagctcaccgtgg ttcagcacaag 2973  
 QY 241 GATTITGCACTGTATTACTGTCACAGTATGTTAGTTCACCTCGGACTTTTGGGACGGG 300  
 Db 2974 accaagtggaactcaaa 2991  
 QY 301 ACCAAGTTGGAGATCAAA 318

RESULT 11  
 ID Q92547 standard; DNA: 6166 BP.  
 AC Q92547:  
 DT 11-MAR-1996 (first entry)  
 DE Expression vector, pPho-TT.  
 KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;  
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;  
 KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;  
 KW alkaline phosphatase; phoA; ss; cyclic.  
 OS Synthetic.  
 PN WO9511317-A1.  
 PD 27-APR-1995.  
 PF 19-OCT-1994; U11907.  
 PR 19-OCT-1993; US-139409.  
 PR 26-APR-1994; US-233619.  
 PR 19-SEP-1994; US-308841.  
 PA (SCRI) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI: 95-170235/22.  
 PT Synthetic human neutralising monoclonal antibodies to human  
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of  
 PT HIV-induced disease  
 PS Example 2; Page 193-197; 249pp; English.  
 CC This sequence represents the expression vector, pPho-TT which is a  
 CC modified version of the phagemid expression vector, pComb3 given in  
 CC Q92546. pPho-TT provides for the expression of soluble Fabs which are  
 CC secreted into the periplasmic space which is regulated from the alkaline  
 CC phosphatase (phoA) promoter. This plasmid was used within the scope of  
 CC the invention to express various mutagenised human Fab's which comprise  
 CC heavy and light variable regions which bind to HIV gp120. pPho-TT  
 CC consists of a DNA molecule having two cassettes to express two soluble  
 CC proteins a heavy chain and a light chain. The vector comprises:  
 CC operatively linked 5' to 3', a first cassette consisting of the phoA  
 CC promoter/operator sequences, an EcoRI restriction site, a ribosome  
 CC binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer  
 CC region, a cloning region bordered by 5' SacI and 3' XbaI restriction  
 CC sites, an NcoI restriction site between the two cassettes, and a second  
 CC cassette consisting of an expression control RBS, a PelB leader, a human  
 CC consensus amino terminus spacer region comprising the sequence EVQLLE,  
 CC a cloning region bordered by 5' XhoI and 3' SpeI restriction sites  
 CC followed by a SfiI site, expression control stop sequences and a NotI  
 CC restriction site. The pPho-TT expression vector contains a light  
 CC chain stuffer that is 1250 bp in length and a heavy chain stuffer that  
 CC is 300 bp in length. The nucleotide sequences of the heavy and light  
 CC chain stuffer encode the heavy and light chain variable domains of a  
 CC tetanus toxin-specific Fab.  
 SQ Sequence 6166 BP; 1418 A 1706 C 1622 G 1115 T

Query Match 82.1%; Score 261; DB 16; Length 6166;

Best Local Similarity 93.4%; Pred. No. 7,78e-158;  
Matches 297; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Db 4607 gaactcacagatcccaagcaccctgtcttctctcaggggaaagagccactctcc 4666  
|||||  
QY 1 GAGTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 50

Db 4667 tccagggccagtcacagatcttaccagccctacttagctctaccagcagaacatggc 4726  
|||||  
QY 61 TCGGTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 120

Db 4727 caggtcccccaggtct 4786  
|||||  
QY 121 CAGTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 180

Db 4787 tccagggccagtcacagatcttaccagccctacttagctctaccagcagaacatggc 4846  
|||||  
QY 181 TCGGTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 240

Db 4847 gatttgcagtcact 4903  
|||||  
QY 241 GATTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 500

Db 4904 accaagtggaactcaaa 4921  
|||||  
QY 301 ACCAAGTGGAGATCAAA 318

RESULT 12  
ID T15203 standard; cDNA: 646 BP.  
AC T15203;  
DE 23-OCT-1996 (first entry)  
KW pc3AP33 anti-tetanus toxoid Ig light chain variable domain cDNA  
KW Mutagenesis: Ig; immunoglobulin FP framework region; variable; CDR.  
KW Complementarity determining region: light; heavy chain; PCR;  
KW polymerase chain reaction; antibody library; diversity; affinity;  
KW immunospecificity; ss.  
OS Synthetic.  
PN WO9607754-A1.  
PD 14-MAR-1996.  
PF 01-SEP-1995; U11235.  
PK 02-SEP-1994; US-A600496.  
PI (Scrib ) SCRIPPS RES INST.  
PI Barbas CF, Burton DR, Lerner RA.  
PI WPI: 96-171625/17  
PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain  
PT gene CDR - useful for prodn. of Ig heavy and light chain  
PT combinatorial antibody libraries  
PS Example 1; Page 84; 125pp; English.  
CC T15203 and T15203 are the heavy and light chain variable domains of  
CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3  
CC based expression vector. The heavy and light chain variable domains  
CC are used in an example to demonstrate the prodn. of antibodies for  
CC an antibody library using mutagenic primers. Mutagenic primers of the  
CC invention have sequences at their 3' and 5' ends both capable of  
CC binding different framework regions linked by a sequence 6 to 50  
CC nucleotides long. Different immunoglobulins produced using the  
CC primers may be used to produce antibody libraries having diverse and  
CC novel immunospecificities and affinities. By using mutagenic ONS an  
CC extremely large population of different randomised binding sites can  
CC be created and use of the universal light chain increases the number  
CC of combinations which yield functional heterodimeric antibodies.  
SQ Sequence 646 BP: 152 A: 187 C: 170 G: 127 T;

Query Match 81.4%; Score 259; DB 22; Length 646;  
Best Local Similarity 93.1%; Pred. No. 1.88e-156;  
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 gactcacagatcccaagcaccctgtcttctctcaggggaaagagccactctcc 60  
|||||  
QY 1 GAGTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 60

Db 61 tccagggccagtcacagatcttaccagccctacttagctctaccagcagaacatggc 120  
|||||  
QY 61 TCGGTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 120

Db 121 caggtcccccaggtct 180  
|||||

|||||  
QY 61 TCGGTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 120

Db 121 caggtcccccaggtct 180  
|||||  
QY 121 CAGTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 180

Db 181 tccagggccagtcacagatcttaccagccctacttagctctaccagcagaacatggc 240  
|||||  
QY 181 TCGGTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 240

Db 241 gatttgcagtcact 247  
|||||  
QY 241 GATTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 300

Db 298 accaagtggaactcaaa 315  
|||||  
QY 301 ACCAAGTGGAGATCAAA 318

RESULT 13  
ID Q70487 standard; cDNA: 646 BP.  
AC Q70487;  
DE 04-APR-1995 (first entry)  
KW Anti-tetanus toxoid light chain cDNA from vector, pc3AP33.  
KW Polymerase chain reaction; primer: mutagenesis; PCR; amplify;  
KW diversity; antibody; complementarity determining region; CDR;  
KW framework; constant; light; heavy; phase; immunoglobulin; library; ss.  
OS Synthetic.  
PN WO9418219-A.  
PD 18-AUG-1994.  
PF 02-FEB-1994; U01234.  
PK 02-FEB-1993; US-012566.  
PR 28-DEC-1993; US-174674.  
PI (Scrib ) SCRIPPS RES INST.  
PI Barbas CF, Burton DR, Lerner RA.  
PI WPI: 94-279673/34.  
PT Oligo-nucleotides - used as PCR primers for producing increased  
PT diversity antibody libraries, for screening antigens  
PS Claim 21; Page 84-85; 120pp; English.  
CC This sequence represents the light chain coding sequence derived from  
CC the surface display phageid expression vector, pc3AP33. pc3AP33  
CC contains the bacteriophage gene III and heavy and light chain variable  
CC domain sequences for encoding human Fab antibodies against tetanus toxin.  
CC This sequence was pref used in the method of the invention for the  
CC production of antibody libraries containing increased diversity. The  
CC sequences given in Q70480-86 are primers which were used for induction  
CC mutagenesis in a complementary determining region (CDR) of an  
CC immunoglobulin light chain gene. These primers contain a 3' terminus  
CC capable of hybridising to a first framework region, a 5' terminus  
CC capable of hybridising to a second framework region and a nucleotide  
CC sequence between the 5' and 3' termini having the formula (NNK)<sub>n</sub>,  
CC where n is 3-24. These primers may be used to produce antibody  
CC libraries with increased antibody diversity by inducing mutagenesis  
CC within the CDR regions of immunoglobulin heavy or light chains that  
CC are displayed on the surface of filamentous phage particles comprising  
CC the library. These primers pref. mutate the light chain CDR3.  
SQ Sequence 646 BP: 162 A: 187 C: 170 G: 127 T;

Query Match 81.4%; Score 259; DB 12; Length 646;  
Best Local Similarity 93.1%; Pred. No. 1.88e-156;  
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 gactcacagatcccaagcaccctgtcttctctcaggggaaagagccactctcc 60  
|||||  
QY 1 GAGTTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 60

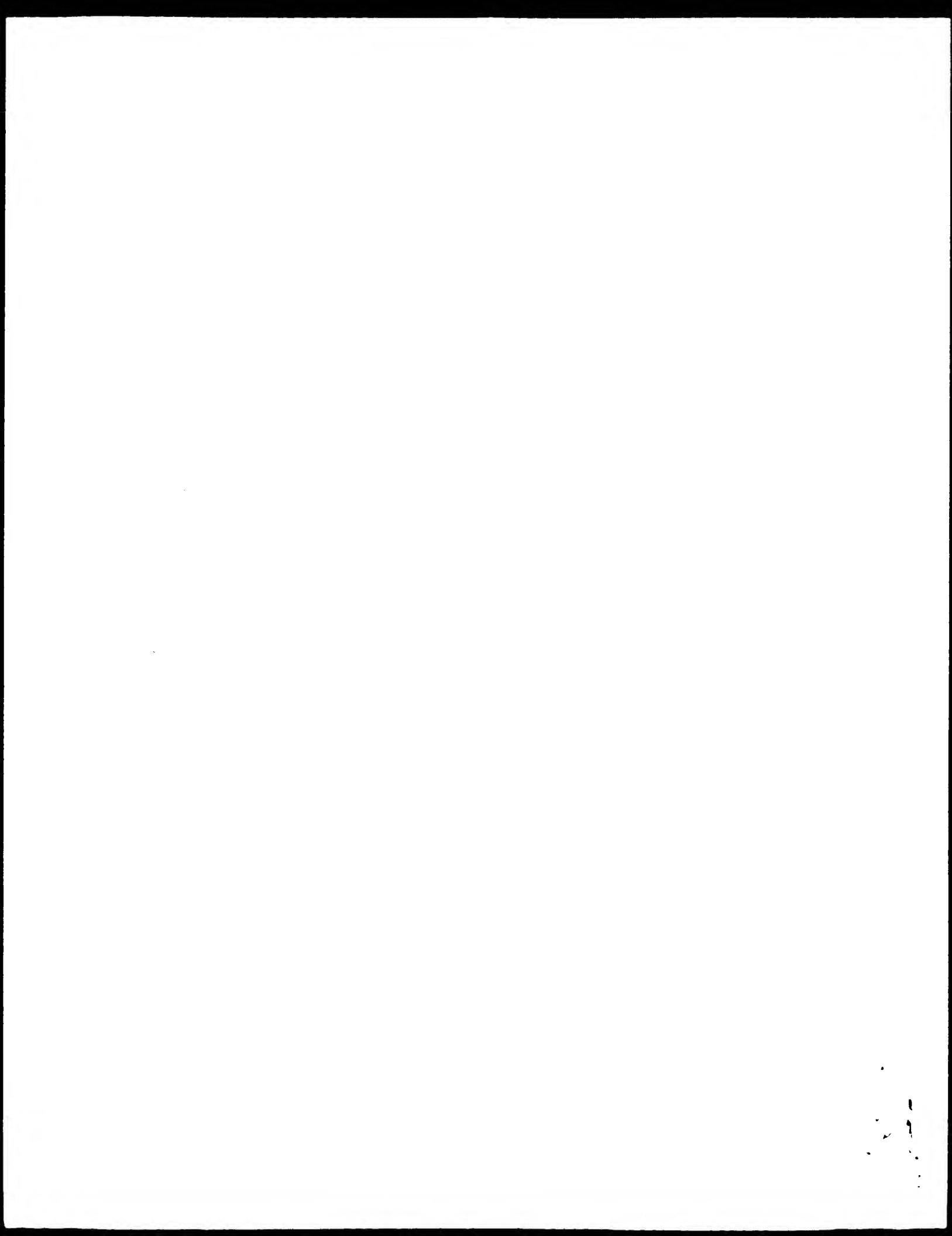
Db 61 tccagggccagtcacagatcttaccagccctacttagctctaccagcagaacatggc 120  
|||||  
QY 61 TCGGTCACGAGTCTCCAGAGTCTCTTCTCTCAGGAAAGAGAGAGAGTCTCC 120

Db 121 caggtcccccaggtct 180  
|||||









# WIREH

(TM)

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MPSrch\_nu n.a - n a database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:45:59 1998: MasPar time 407 74 Seconds  
Tabular output not generated 1107.744 Million cell updates/sec

Title: >US-08-844-215-17  
Description: (1-118) from US08044215 seq  
Perfect Score: 318  
N.A. Sequence: 1 GAGTCACCGACGCTCTCAGG GAGCAAGTTCAGATCAAA 318  
Comp: GTCAGTCTCTCAGCAAGTCTC

Scoring table: TABLE default  
Gap 5  
Nmatch STD : Dbase 0: Query 0  
Searched: 43261 seqs 71021776 bases x 2  
Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: emb1-new7  
1-BCT 2-PUN 3-GEN 4-HTG1 5-HTG2 6-HTG3 7-HTG4 8-HTM1  
9-HUM2 10-HUM3 11-INV1 12-INV2 13-ORG 14-MAX 15-VPT  
16-PLN 17-PP1 18-PP2 19-PP3 20-SYN 21-UNC 22-VIP  
Database: genbank101  
23-BCT1 24-NC12 25-RC13 26-RC14 27-RC15 28-RC16 29-RC17  
30-BCT8 31-BCT9 32-BCT10 33-BCT11 34-BCT12 35-BCT13  
36-GEN1 37-GEN2 38-GEN3 39-GEN4 40-GEN5 41-GEN6 42-HTG1  
43-HTG2 44-HTG3 45-HTG4 46-HTG5 47-INV1 48-INV2 49-INV3  
50-INV4 51-INV5 52-INV6 53-INV7 54-INV8 55-INV9 56-INV10  
57-INV11 58-INV12 59-MAM1 60-MAM2 61-MAM3 62-VPT1  
63-VPT2 64-VPT3 65-VPT4 66-PAT1 67-PAT2 68-PAT3 69-PAT4  
70-PAT5 71-PAT6 72-PAT7 73-PHC 74-PLN1 75-PLN2 76-PLN3  
77-PLN4 78-PLN5 79-PLN6 80-PLN7 81-PLN8 82-PLN9 83-PLN10  
84-PLN11 85-PLN12 86-PLN1 87-PLN2 88-PLN3 89-PLN4  
90-PLN5 91-PLN6 92-PLN7 93-PLN8 94-PLN9 95-PLN10  
96-PLN11 97-PLN12 98-PLN13 99-PLN14 100-PLN15 101-PLN16  
102-PP17 103-PP18 104-PP19 105-PP20 106-PP21 107-PP22  
108-PP23 109-PP24 110-PP25 111-PP26 112-PP27 113-SYN  
114-UNA  
Database: genbank101  
115-VPL1 116-VPL2 117-VPL3 118-VPL4 119-VPL5 120-VPL6  
121-VPL7 122-VPL8 123-VPL9 124-VPL10 125-VPL11  
Database: genbank-new7  
126-BCT 127-GEN 128-HTG1 129-HTG2 130-INV 131-MAX  
132-VPT 133-PHC 134-PLN1 135-PLN2 136-PLN3 137-PP12  
138-ROD 139-SYN 140-UNA 141-VRL  
Database: u-emb151101  
142-part1 143-part2

Statistics: Mean 9.97 Variance 4.54 scale 2.107  
Pred NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	294	92.5	387	90	HSBUD45L	H.sapiens mRNA for an	3,316-216
2	292	91.8	387	90	HUMIGKAF	Human Ig rearranged k	2,338-214
3	292	91.8	387	90	HSS1PVL	H.sapiens immunoglobulin	2,338-214
4	290	91.2	320	99	HUMICKAQ	Human Ig rearranged k	1,590-212
5	290	91.2	324	91	HSIGVLTID	H.sapiens mRNA for Ig	1,636-212
6	290	91.2	324	91	HSIGVKT3C	H.sapiens mRNA for Ig	1,636-212
7	290	91.2	447	92	HUMIGHRA	Human Ig rearranged k	1,636-212
8	288	90.6	402	91	HSYKAVIC	Human mRNA for Ig k	1,370-211
9	288	90.6	320	99	HUMIGKAT	Human Ig rearranged k	1,146-210
10	288	90.6	324	95	HSY766B2	Human Ig rearranged k	1,146-210
11	288	90.6	402	99	HUMICKAI	Human Ig active kappa	1,146-210
12	288	90.6	402	91	HSIGKVAH	Human mRNA for Ig k	1,346-210
13	287	90.3	324	99	HUMICKVS	Human sapsins for kappa	9,596-210
14	286	89.9	324	99	HUMIKH1RA	Human sapsins (alpha1)	8,000-210
15	286	89.9	324	99	HUMAB55	Human immunoglobulin	8,000-210
16	286	89.9	364	99	HUMIGL3AC	Human Ig rearranged k	8,000-210
17	284	89.3	300	99	HUMICKOB	Human sapsins (clone 1)	8,000-210
18	284	89.3	318	99	HUMIGKVS	Human sapsins (clone 1)	8,000-210
19	284	89.3	329	91	HSIGRHE19	H.sapiens (HFM16K) m	5,596-210
20	283	90.0	312	91	HSIGRHE18	H.sapiens (HFM13K) m	4,596-210
21	284	89.9	318	91	HSIGKHE20	H.sapiens (HFM28K) m	4,596-210
22	282	88.7	323	99	HUMIGKAF	Human Ig rearranged k	3,916-210
23	282	88.7	360	99	HUMIGHE1	Human Ig rearranged k	3,916-210
24	280	88.1	300	99	HUMICKOP	Human sapsins (clone 1)	2,736-210
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26	278	87.4	300	99	HUMICKOF	Human sapsins (clone 1)	1,900-211
27	278	87.4	324	94	HSY034P3	Human clone 354 k	1,900-211
28	278	87.4	307	96	HSY74667	H.sapiens mRNA for m	1,900-211
29	278	87.4	327	99	HUMIGLVRD	Human immunoglobulin	1,900-211
30	278	87.4	330	98	HUMABFGLJ	Human Fab fragment b1	1,900-211
31	278	87.4	330	98	HUMABFGLB	Human Fab fragment b1	1,900-211
32	278	87.4	387	98	HUMIGL14L	Human sapsins Ig rearr	1,900-211
33	278	87.4	387	97	HUMANTIGPA	Human anti-glycoprotein	1,900-211
34	278	87.4	429	91	HSIGK375A	H.sapiens rearranged	1,900-211
35	277	87.1	324	98	HUMHETPSAL	Human hepatitis B sur	1,900-211
36	277	87.1	333	95	HSY2772	Human anti-HIV-1 p12	1,900-211
37	276	86.8	300	99	HUMICKOB	Human sapsins (clone 1)	1,320-210
38	276	86.8	324	94	HSY03462	Human clone 284 k	1,320-210
39	276	86.8	326	99	HUMIGLRFM	Human sapsins (H0471)	1,320-210
40	276	86.8	326	99	HUMIGLRFI	Human sapsins (H0471)	1,320-210
41	276	86.8	327	102	S61031	Ig V kappa 112.1 kDa	1,320-210
42	276	86.8	327	98	HUMABFGLH	Human Fab fragment b1	1,320-210
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44	276	86.8	323	91	HSIGK2BS1	H.sapiens rearranged	1,320-210
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## ALIGNMENTS

RESULT 1 HSBUD45L 387 bp RNA 27-MAR-1994  
LOCUS H.sapiens mRNA for anti-HSV antibody VL chain (V kappa 17) kappa 21  
DEFINITION Z46345  
ACCESSION  
KEYWORDS anti-HSV antibody; immunoglobulin kappa chain; immunoglobulin light chain; joining region; variable region.  
SOURCE Human.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 387)  
AUTHORS Mahmoodi, M., Edwards, J., Cairns, E. and Bell, D.  
TITLE Molecular characterization of natural human anti-HSV ant antibodies  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 387)  
AUTHORS Mahmoodi, M.

TITLE Direct Submission  
JOURNAL Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario,  
Medicine and Microbiology and Immunology, University Hospital Room  
BRE-12, London, Ontario, Canada, N6A 5A5

## FEATURES

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QY 307 TTGGAGATCAAA 318

RESULT 2 HUMIGKAR 320 bp DNA PRI 04-JAN-1995  
LOCUS Human Ig rearranged kappa chain V-J2-region gene, partial cds.  
DEFINITION M28167  
ACCESSION g185908  
NID  
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;  
Immunoglobulin-kappa.  
SOURCE Human lymphocyte DNA, from patient BRA with small lymphocytic  
lymphoma and associated chronic lymphocytic leukemia.  
ORGANISM Homo sapiens  
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Euthera; Primates, Catarrhini, Hominoidea, Homo.  
REFERENCE 1 (bases 1 to 320)  
AUTHORS Pratt J F., Passenti L., Larrick J., Robbins, R., Ranks, P. M. and  
Kipps, T. J.  
TITLE Ig V region gene expression in small lymphocytic lymphoma with

little or no somatic hypermutation  
J. Immunol. 143 (2): 65d-7n5 (1989)  
89292697  
MEDLINE  
COMMENT Draft entry and printed sequence for [1] kindly submitted by  
L F Pratt, 20-SEP-1989

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QY 127 CCCAGGCTCTCATCTATGTTGTTATCCAGCAGGCGGCTGCTGCTCCAGACAGAGTTCAT 186  
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QY 307 TTGGAGATCAAA 318

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ACCESSION 9601982  
NID  
KEYWORDS Immunoglobulin; kappa chain; V-J region.  
SOURCE Human.  
ORGANISM Homo sapiens  
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 330)  
AUTHORS Chapman, C. J., Spellerberg, M. B., Hamblin, J. J. and Stevenson, F. K.  
TITLE Pattern of usage of the VH4-21 gene by B lymphocytes in a patient  
with EBV infection indicates ongoing mutation and class switching  
JOURNAL Mol. Immunol. 32 (5): 347-353 (1995)  
MEDLINE 95257976  
REFERENCE 2 (bases 1 to 330)  
AUTHORS Chapman, C. J.



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DEFINITION H.sapiens mRNA for Ig kappa light chain variable region
(V-J), subgroup III (clone C3).
ACCESSION X73863
NID 9516187
KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup III;
Ig variable region; immunoglobulin.
SOURCE Homo sapiens
ORGANISM
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
Colls, J.C., Pegg, C.A.S., Rees-Smith, B., and Burton, D.R.,
TITLE Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Hexham, J.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western
Bank, Sheffield S10 2UH, UK
REFERENCE 3 (bases 1 to 324)
AUTHORS Hexham, J.M., Furmaniak, J., Pegg, C., Burton, D.R. and Smith, R.P.
TITLE Cloning of a human autoimmune response preparation and sequencing
of a human anti-thyroglobulin autoantibody using a combinatorial
approach

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Autoimmunity 12 (2), 135-141 (1992)
JOURNAL 92314301
MEDLINE 4 (bases 1 to 324)
REFERENCE Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
AUTHORS Colls, J.C., Pegg, C., Rees-Smith, B. and Burton, D.R.,
TITLE Cloning and characterisation of 170 autoantibodies using
combinatorial phage display libraries
JOURNAL Autoimmunity 17 (3), 167-179 (1994)
MEDLINE 95035699
FEATURES
Location/Qualifiers
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DEFINITION Human Ig rearranged gamma-chain MPNA V-region, partial cds.
ACCESSION L03162
NID g185397
KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to
mRNA.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Collier, I.A., Boden, P., O'Kennedy, P., Barbas, C.F. III, Burton, D.R.
and Lerner, P.A.
TITLE A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10798-10800 (1992)
MEDLINE 93066172
FEATURES Location/Qualifiers

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REFERENCE 1 (bases 1 to 320)
AUTHORS Pratt, L.F., Passentini, J., Larrick, J., Robbins, E., Banks, P.M., and
        Kipps, T.J.
TITLE Ig V region gene expression in small lymphocytic lymphoma with
        little or no somatic hypermutation
JOURNAL J. Immunol. 143 (2): 699-705 (1989)
MEDLINE 89292597
COMMENT Draft entry and printed sequence for [1] kindly submitted by
        L.F. Pratt, 20-Sep-1989.
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DEFINITION 076682
ACCESSION 076682
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
        Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS 1 (bases 1 to 324)
TITLE Ig V region gene usage by autoreactive MoAbs
JOURNAL Unpublished

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REFERENCE 2 (bases 1 to 324)
AUTHORS Aguilera, I.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1996) Aguilera I., Hospital U Virgen del Rocío,
        Immunology, Manuel Siurot s/n, Seville, Spain, 41013
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Best Local Similarity 96.2%; Pred. No. 1.14e-230;
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DEFINITION M27025
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NID g185845
KEYWORDS C-region; V-region; immunoglobulin light chain;
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ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
        Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS 1 (bases 1 to 402)
TITLE Molecular characterization of a major autoantibody-associated
        cross-reactive idiotype in Sjogren's syndrome
JOURNAL J. Immunol. 142, 4261-4268 (1989)
MEDLINE 89256674
COMMENT Draft entry and printed copy of sequence kindly submitted by
        T.J. Kipps, 16-AUG-1989.
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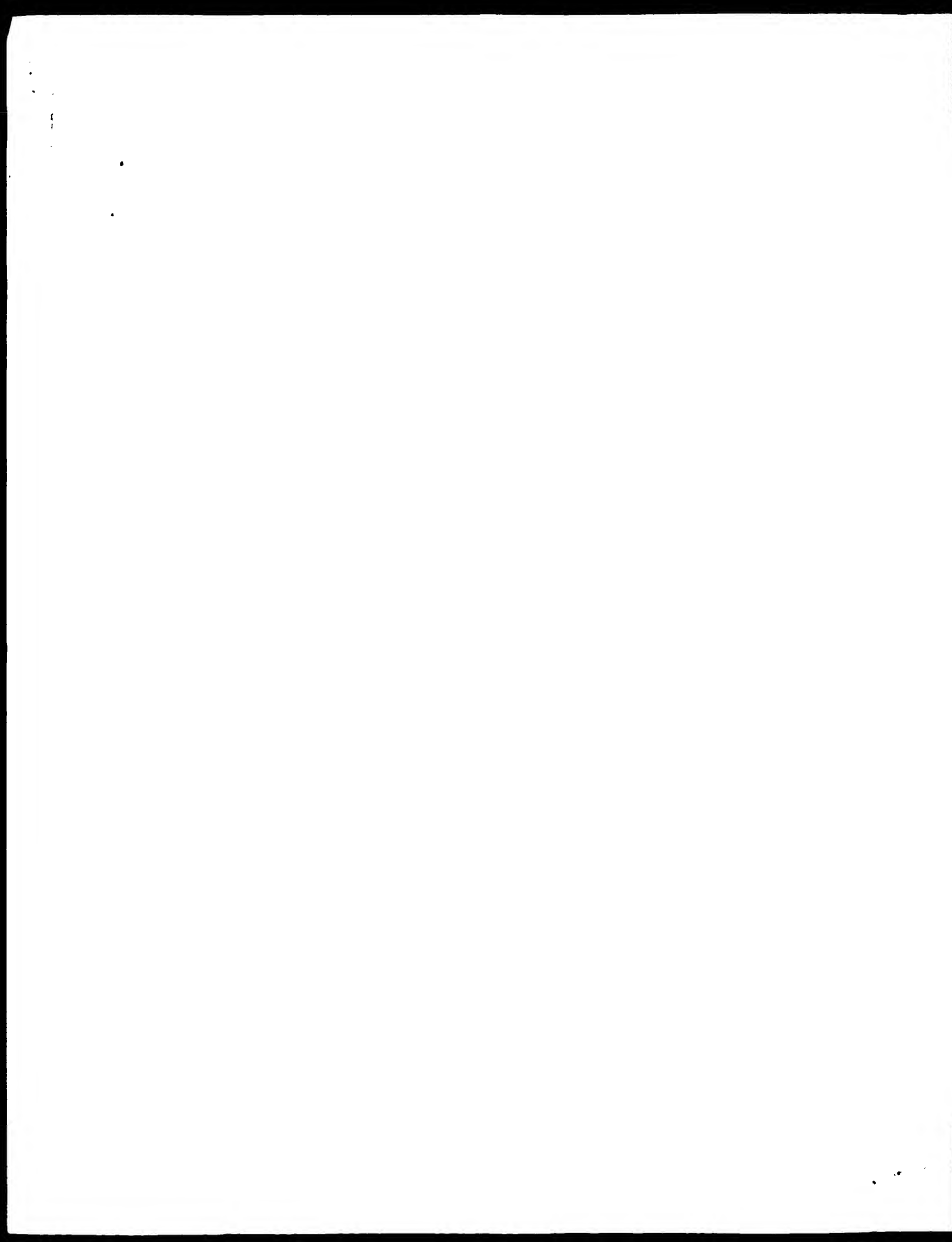
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Db 73 gccagtcagatgtttacagacagctactttagctgttaccagcaaaacctgaccagct 132
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QY 67 GCCAGTCAAGAGTATAGSAGCAACIACIIAGCTGTGTACAGCAAAAAACCTGGCCAGCT 126
   |||||||
Db 133 cccaaagctccctcactcactcagtcacacagagagccactgacatccacagacaggttcagt 192
   |||||||
QY 127 CCAACACCTCTATCTATAGGTATATATAGAGAGCACTGGATATCCAGAAAGAGGTTCAGT 186
   |||||||
Db 193 ggcagtgagctcagagacactcactcaccatcaccagcagcagcctgagccctgaagatctt 252
   |||||||
QY 187 GGTATATAGGTATAGAGACACTTTCATCTTCACATACAGCACTGGAGCTGAGAGATTTT 246
   |||||||
Db 253 gcaagtattactcagagagatattgttagctacccgagagacgttcggccaaagagaccag 312
   |||||||
QY 247 GCAGTGATATACCTGACAGATATAGTATAGCTTTCAGATTTTGGGCAAGAGAGAGCAAG 306
   |||||||
Db 313 atggaatcaaa 324
   |||||
QY 307 TTGAGATCAAA 318

```

Search completed: Tue Feb 24 07:55:19 1998  
 Job time : 560 secs.



# WATERMAN

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MPSrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:42:43 1998. MaxFst: time 110.86 seconds  
710,002 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-16  
Description: (1-312) from US08844215.seq  
Percent Score: 312  
N.A. Sequence: 312 1 GAGCTCAGTCACTGATCTCTCTAGC  
Comp: CTTGGATGAGAGAGAGAGAGAGAG

Scoring table: TABLE default  
Gap 5

Nmatch STD: Kruse 0. Query 0

33433 seqs, 126143548 bases x 2

Post-processing: Minimum Match 04  
Listing first 45 summaries

Database: STS

1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8  
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14  
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19 20:STS20  
21:STS21 22:STS22 23:STS23 24:STS24 25:STS25 26:STS26  
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82:STS82 83:STS83 84:STS84 85:STS85 86:STS86 87:STS87  
88:STS88 89:STS89 90:STS90 91:STS91 92:STS92 93:STS93  
94:STS94 95:STS95

Statistics: Mean 9.886; Variance 1.971; scale 5.015

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES			
Result No.	Score	Length DR ID	Description
1	202	54.7	400 50 HSL144450
2	176	56.4	432 33 AAC15509

3	176	56.4	418 71 HSL1308877
4	164	52.6	242 26 AA179557
5	164	52.6	242 34 HSL128912
6	164	52.6	242 63 HSL128912
7	164	52.6	242 63 HSL128912
8	164	52.6	242 63 HSL128912
9	164	52.6	242 63 HSL128912
10	164	52.6	242 63 HSL128912
11	164	52.6	242 63 HSL128912
12	164	52.6	242 63 HSL128912
13	164	52.6	242 63 HSL128912
14	164	52.6	242 63 HSL128912
15	164	52.6	242 63 HSL128912
16	164	52.6	242 63 HSL128912
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41	164	52.6	242 63 HSL128912
42	164	52.6	242 63 HSL128912
43	164	52.6	242 63 HSL128912
44	164	52.6	242 63 HSL128912
45	164	52.6	242 63 HSL128912

RESULT 1  
ID HSL144450 standard; RNA: EST: 400 BP.  
AC AA456778;  
NI 92177199  
DT 07-JUN-1997 (Ref 52, Created)  
DT 07-JUN-1997 (Ref 52, Last updated, Version 1)  
DE 2427111111 Soares ovary tumor NbrCT Homo sapiens cDNA clone 770541  
DE 5' similar to gb:X08764 IG KAPPA CHAIN PPTCPSPOR V-111 REG1N  
DE (HUMAN).  
KW EST.  
OS Homo sapiens (human)  
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
RN [1]  
RP 1-400  
PA Hillier L., Allen M., Bowles I., Dubouque T., Gaisel G., Jost S.,  
PA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,  
PA Moore R., Schellenberg K., Steptoe M., Tan F., Theisand J.,  
PA White Y., Wyllie T., Waterston R., Wilson R.,  
PA "WashU-Merck EST Project 1997";  
RL Unpublished.  
CC Contact: Wilson PK WashU-Merck EST Project Washington University  
CC School of Medicine 4444 Forest Park Parkway, Box 4501, St. Louis,  
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
CC estw@wustl.edu This clone is available royalty-free through  
CC LNL. Contact the WASHU Consortium (info@wustl.edu) for

## ALIGNMENTS

CC further information. Trace considered overall poor quality Seq  
 CC primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.  
 FH Key Location/Qualifiers  
 FT source  
 FT 1..400  
 FT /organism="Homo sapiens"  
 FT /note="organ: ovary; Vector: pT73D (Pharmacia) with a  
 FT modified polylinker; Site1: Not I; Site2: Eco RI; 1st  
 FT strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 FT TGTTACCAATCTGAAGTCGGAGCGCGGTTTCTTTTCTTTTCTTTT  
 FT 3']  
 FT double-stranded cDNA was size selected, ligated to Eco RI  
 FT adaptors (Pharmacia), digested with Not I and cloned into  
 FT the Not I and Eco RI sites of a modified pT73 vector  
 FT (Pharmacia). Library constructed by Bento Soares and  
 FT M Fatima Bonaudo  
 FT /clone="770541"  
 FT /clone.lib="Soares ovary tumor NBH0T"  
 FT /sex="female"  
 FT /tissue.type="ovarian tumor"  
 FT /lab\_host="DH10B (ampicillin resistant)"  
 FT <1..>400  
 FT mRNA  
 FT Sequence 400 BP: 90 A: 120 C: 106 G: 84 T: 0 other:  
 SQ

Query Match 64.7%; Score 202; DB 60; Length 400;  
 Best Local Similarity 87.9%; Pred No 0.00e+00;  
 Matches 275; Conservative 0; Mismatches 31; Indels 7; Gaps 5:

Db 70 acgagctccagggaccctgttctgtccaggggaaagagccacctctctcagg 129  
 QY 7 ACTCAGTCTCCAGCCACCTGCTTTGTCTCCAGGGGAAAGAGCCACCTCTCCTG 66

Db 130 qcagctcacagctgttagcagcagctgcttagcctggtaccagcagaaacctggccagct 189  
 QY 67 GCCAGTCACAGTGTAAACA--AG-TACTAGCTGTGTACCAAGCAACCTTGGCCAGGCT 123

Db 190 ccagagctcctctatctggtgcaccagcaggcgaactggcctccagcagcagcttcagct 249  
 QY 124 CCCAGGCTCTCATCTATCATGATCCCAACAGGAGGCTATGTCATCCCAAGTCAGTTCAGT 183

Db 250 qgcagtggtctgagcagcagctcctctcctcagcagcagcagcagcagcagcagctt 309  
 QY 184 GGCAGTGGTGTCTGGGACAGATTTCACTTCACTATGACAACTGTAGAGCTT 242

Db 310 tgcagtgattactgcagcagctggttagctccacgctggcagcagcagcagcagcagc 369  
 QY 243 TGCATTTTATTACTGTCAGCAGCTAGGCACTGG--GTC-ATTTCGCGCGAGGAGCAACAA 299

Db 370 ggtggaaatcaaa 382  
 QY 300 GGTGGAGATCAAA 312

RESULT 2  
 LOCUS AA515239 418 bp mRNA EST 14-JUL-1997  
 DEFINITION g959c07.s1 NCI\_CGAP\_Lip2 Homo sapiens cDNA clone 940044 similar to  
 gb:M63438 IG KAPPA CHAIN PRECUPSOR V-III REGION (HUMAN);  
 ACCESSION AA515239  
 NID 92254839  
 KEYWORDS EST  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
 Homo.  
 REFERENCE 1 (bases 1 to 418)  
 AUTHORS NCI-CGAP.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 JOURNAL Tumor Gene Index  
 COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Krizman, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LCNC at:  
 www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd, ET from Amersham  
 High quality sequence stop: 413.

#### FEATURES

source  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /note="Vector: pAMP10; mRNA made from liposarcoma. cDNA  
 made by oligo-dT priming. Non-directionally cloned.  
 Size-selected on agarose gel, average insert size 600 bp.  
 Reference: Krizman et al. (1996) Cancer Research  
 56:5380-5383.  
 /clone="940044"  
 /clone.lib="NCI\_CGAP\_Lip2"  
 /tissue\_type="liposarcoma"  
 /lab\_host="DH10B"  
 <1..>418

BASE COUNT 90 a 127 c 102 g 90 t  
 ORIGIN

Query Match 56.4%; Score 176; DB 39; Length 419;  
 Best Local Similarity 87.7%; Pred No 3.59e+297;  
 Matches 228; Conservative 0; Mismatches 28; Indels 4; Gaps 3:

Db 95 acgagctccagcagcagcctgttctctccaggggaaagagcaccctctcttcagc 154

QY 7 ACTCAGTCTCCAGCCACCTGCTTTGTCTCCAGGGGAAAGAGCCACCTCTCTGTAAG 66

Db 155 gcaagctcagctatccatcagcagcagccttagcctggtatcagcaaaacctggccagct 214

QY 67 GCCAGTCACAGTGTAAACA--AGTAC-TTAGCTGTGTACCAACAGAACTGCCAGGCT 123

Db 215 cccaggtcctctatctcagtggtgcatacagcagggccactgg-ctcccagcagcagctc 273

QY 124 GGCAGGCTCTCTCATCTATGATGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 183

Db 274 gcaagctcgtcggagcagcagctcagctcaccatgcagcagcagcagcagcagct 333

QY 184 GGCAGTGGGTTGTGGACAGAGCTTCTCTCAGCAACAGCAACAGCAACAGCAACAG 243

Db 334 gcagtttactattgtcagca 353

QY 244 GCAGTTTATTACTGTCAACA 263

#### RESULT 3

ID HS1308877 standard; RNA; EST; 418 BP.

AC AA515239;

NI 92254839

DT 15-JUL-1997 (Rel. 52, Created)

DT 24-JUL-1997 (Rel. 52, Last updated, Version 2)

DE g959c07.s1 NCI\_CGAP\_Lip2 Homo sapiens cDNA clone 940044 similar to

DE gb:M63438 IG KAPPA CHAIN PRECUPSOR V-III REGION (HUMAN);

KW EST.

OS Homo sapiens (human)

OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

OC Homo.

RN [1]

RP 1-418

RA NCI-CGAP;

RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP)."

RT Tumor Gene Index;

RL Unpublished.

CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:

CC Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,















\*\*\*\*\*  
WIREHOLE  
\*\*\*\*\*  
(TM)

Release 2 ID John F. Collins, Biocomputing Research Unit  
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Distribution rights by IntelliGenetics, Inc.  
MFSrch\_00 n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:39:26 1998; MaxPar time 107.92 Seconds  
Tabular output not generated.  
Title: >US-08-844-215-15  
Description: (1-312) from US08844215.seq  
Perfect Score: 312 1 GAGCAGTACCTGACCTGACG  
N.A. Sequence: 1 GAGCAGTACCTGACCTGACG  
Comp: CTCGAGTACCTGACCTGACG

Scoring tables: TABLE default  
Gap 6  
Nmatch STD : Dbase 0; Query 0  
Searched: 39746 seqs, 1410104 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: EST-C  
1:EST107 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202  
7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208  
13:EST209 14:EST210 15:EST211 16:EST212 17:EST213  
18:EST214 19:EST215 20:EST216 21:EST217 22:EST218  
23:EST219 24:EST220 25:EST221 26:EST222 27:EST223  
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73:EST269 74:EST270 75:EST271 76:EST272 77:EST273  
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83:EST279 84:EST280 85:EST281 86:EST282 87:EST283  
88:EST284 89:EST285 90:EST286 91:EST287 92:EST288  
93:EST289 94:EST290 95:EST291 96:EST292 97:EST293  
98:EST294  
EST-D  
99:EST295 100:EST296 101:EST297 102:EST298 103:EST299  
104:EST300 105:EST301 106:EST302 107:EST303 108:EST304  
109:EST305 110:EST306 111:EST307 112:EST308 113:EST309  
114:EST310 115:EST311 116:EST312 117:EST313 118:EST314  
119:EST315

Statistics: Mean 9.871; Variance 1.938; scale 5.0q3  
Pred. No is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	224	71.8	328	24	AA295311	EST100471 Pancreas tu
2	218	69.9	370	24	AA295093	EST100400 Pancreas tu
3	212	67.9	345	59	AA457044	EST10446 Skin tumor 1
4	202	64.7	400	116	AA457078	EST10446 Skin tumor 1
5	189	63.5	346	25	AA300582	EST13427 Testis tumor
6	188	63.5	346	25	AA300582	EST13427 Testis tumor
7	189	60.6	405	52	AA367405	EST174511 Pancreas tum
8	188	60.6	405	52	AA367405	EST174511 Pancreas tum
9	188	60.6	405	52	AA367405	EST174511 Pancreas tum
10	163	52.0	283	53	AA457078	EST10446 Skin tumor 1
11	159	51.0	253	25	AA395941	EST101165 Thyroid 11
12	157	50.3	218	62	AA382014	EST1387 Thyroid 11
13	155	49.7	277	24	AA395377	EST100538 Pancreas tu
14	152	48.7	294	37	AA327218	EST10586 Colon 1 Homo
15	152	48.7	294	37	AA327218	EST10586 Colon 1 Homo
16	152	48.7	294	37	AA327218	EST10586 Colon 1 Homo
17	151	48.4	294	35	AA366451	EST17408 Pancreas tum
18	148	47.4	255	92	AA384652	EST100323 Pancreas tu
19	148	47.4	255	92	AA384652	EST100323 Pancreas tu
20	145	46.8	253	100	AA291691	EST100323 Pancreas tu
21	140	44.9	244	86	AA430565	EST100323 Pancreas tu
22	138	44.2	249	79	AA432152	EST100323 Pancreas tu
23	137	43.9	249	79	AA432152	EST100323 Pancreas tu
24	135	43.6	259	87	AA434001	EST100323 Pancreas tu
25	134	42.9	255	100	AA291691	EST100323 Pancreas tu
26	132	42.3	252	27	AA301361	EST14181 Testis tumor
27	130	41.7	252	27	AA301361	EST14181 Testis tumor
28	126	40.4	413	27	AA301347	EST10400 T-cell lymph
29	123	40.1	382	25	AA395386	EST14272 Testis tumor
30	124	39.7	382	25	AA395386	EST14272 Testis tumor
31	122	39.1	304	100	AA291691	EST100323 Pancreas tu
32	122	39.1	304	100	AA291691	EST100323 Pancreas tu
33	116	37.2	250	72	AA300371	EST13604 T-NCI CHAP P
34	116	37.2	250	72	AA300371	EST13604 T-NCI CHAP P
35	112	35.9	334	37	AA327254	EST10547 Colon 1 Homo
36	112	35.9	334	37	AA327254	EST10547 Colon 1 Homo
37	110	35.6	303	26	AA300598	EST100323 Pancreas tu
38	109	34.9	303	26	AA300598	EST100323 Pancreas tu
39	107	34.3	292	24	AA395388	EST13847 Testis tumor
40	105	34.0	301	58	AA377395	EST100751 Pancreas tu
41	105	34.0	301	58	AA377395	EST100751 Pancreas tu
42	93	32.4	196	55	AA366724	EST168837 Small intest
43	93	32.4	196	55	AA366724	EST168837 Small intest
44	95	30.4	282	26	AA300342	EST13454 Testis tumor
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54	95	30.4	282	26	AA300342	EST13454 Testis tumor
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92	95	30.4	282	26	AA300342	EST13454 Testis tumor
93	95	30.4	282	26	AA300342	EST13454 Testis tumor
94	95	30.4	282	26	AA300342	EST13454 Testis tumor
95	95	30.4	282	26	AA300342	EST13454 Testis tumor

ALIGNMENTS

RESULT	LOCUS	328 bp	mrna	EST	18-APP-1997
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DEFINITION	Immunoglobulin kappa light chain, VJ regions.				
ACCESSION	AA295311				
NID	g1947646				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotic; mitochondrial eukaryotes; Metazoa; Chordata;				
AUTHORS	Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Homnidae;				
	Homo.				
	1 (bases 1 to 328)				
	Adams, M.P., Verlaage, A.P., Fleischmann, P.D., Fuldner, K.A.,				
	Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Socolay, J.D.,				
	White, C., Sutton, G., Blake, J.A., Brandon, R.C., Mac-Wal, C.,				
	Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.B.,				
	Flitcald, L.M., Fitzhugh, W.M., Frichman, J.B., Goodham, N.S.,				
	Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkie, P., Joffe,				

Kelley, J. M., Kelley, J. C., Liu, L. T., Marmaros, S. M., Merrick, J. M., Moreno-Palauques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. P., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Weissner, P. S., Olsen, H., Paymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Posen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

**TITLE**  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

**JOURNAL**  
Nature 377 (6547 Suppl), 3-174 (1995)

**MEDLINE**  
96026280

**COMMENT**  
Other ESTs: THC169106  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi.html>)  
Seq primer: M13 Reverse.

**FEATURES**  
source  
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/organism="Homo sapiens"  
/note="Organ: pancreas, Vector: pBluescript SK-, Site\_1:  
ECORI, Site\_2: XhoI"  
/clone\_lib="Pancreas tumor I"  
/dev\_stage="adult"  
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73 a 93 c 78 g 77 t 7 others

**BASE COUNT**  
73 a 93 c 78 g 77 t 7 others

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71.88; Score 224; DB 24; Length 328;  
Best Local Similarity 90.08; Pred. No. 0.00e+00;  
Matches 244; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 52 acgagnttcacgacccctgtgtgttcagggaagagccacccttcctgcagg 111  
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QY 7 ACTGAGTCTCAGGCTCCTGCTGTTTGTCTCAGGAGGAAAGAGCCCTCTCTGTCAGS 66  
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Db 112 gccagtcagagtgtagcagcaacttagcctggtaccagcagaacccctggccaggtccc 171  
|||||  
QY 67 GCCAGTCAGAGTGTAAACAGTACTTAGCTGTGTACACAGAGAAACCTGGCCAGGCTCC 126  
|||||

Db 172 aggtcctcatctatgtgtcatccatcagggnccactggccatcccagcaggttcagtgcc 231  
|||||  
QY 127 AGGCTCTCATCTATGATGATCCACAGGGGCACCTGGGATCCAGGACAGGTTTCAAGTGGC 186  
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Db 232 agtgggtctgggacagagttcactctcancatcagcatcctgcagctcgaagatttnc 291  
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QY 197 AGTGGTCTGGACAGACTTCACTCTCACCATCAGCAACCTAGAGGCTGAAGATTITGCA 245  
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Db 292 gttattactgtcagcagtaataaactagg 322  
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QY 247 GTTTATTACTGTACGACGCTAGCGACTGG 277  
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**RESULT**  
2 AA295093 370 bp mRNA EST 18-APR-1997  
LOCUS EST106400 pancreas tumor I Homo sapiens cDNA 5' end similar to  
DEFINITION Similar to immunoglobulin kappa, variable region (GB:Y00640).  
ACCESSION AA295093  
NID g1947582  
KEYWORDS EST.  
SOURCE human.  
\* ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

**REFERENCE**  
AUTHORS  
1 (bases 1 to 370)  
Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Feldner, R. A., Bult, C. J., Lee, N. H., Kirkness, F. F., Weinstock, K. G., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Wai, C., Clayton, P. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Frichman, J. L., Geughagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. T., Marmaros, S. M., Merrick, J. M., Moreno-Palauques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. P., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Weissner, P. S., Olsen, H., Paymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

**TITLE**  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

**JOURNAL**  
Nature 377 (6547 Suppl), 3-174 (1995)

**MEDLINE**  
96026280

**COMMENT**  
Other ESTs: THC168243  
Contact: Kerlavage, AR  
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Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi.html>)  
Seq primer: M13 Reverse.

**FEATURES**  
source  
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/organism="Homo sapiens"  
/note="Organ: pancreas, Vector: pBluescript SK-, Site\_1:  
ECORI, Site\_2: XhoI"  
/clone\_lib="Pancreas tumor I"  
/dev\_stage="adult"  
1..370  
85 a 107 c 94 g 77 t 7 others

**BASE COUNT**  
85 a 107 c 94 g 77 t 7 others

**Query Match**  
69.98; Score 218; DB 24; Length 370;  
Best Local Similarity 90.58; Pred. No. 0.00e+00;  
Matches 237; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 59 acgcannttcagcagccctgtcgtgtgttcagggaagagccaccctctcctgagg 118  
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QY 7 ACTGAGTCTCAGGCTCCTGCTGTTTGTCTCAGGAGGAAAGAGCCCTCTCTGTCAGS 66  
|||||

Db 119 gccagtcagagtgtagcagcaacttagcctggtaccagcagaacccctggccaggtccc 178  
|||||  
QY 67 GCCAGTCAGAGTGTAAACAGTACTTAGCTGTGTACACAGAGAAACCTGGCCAGGCTCC 126  
|||||

Db 179 aggtcctcatctatgtgtcatccatcagggnccactggccatcccagcaggttcagtgcc 238  
|||||  
QY 127 AGGCTCTCATCTATGATGATCCACAGGGGCACCTGGGATCCAGGACAGGTTTCAAGTGGC 186  
|||||

Db 239 agtgggtctgggacagagttcactctcancatcagcatcctgcagctcgaagatttnc 298  
|||||  
QY 187 AGTGGTCTGGACAGACTTCACTCTCACCATCAGCAACCTAGAGGCTGAAGATTITGCA 245  
|||||

Db 299 gttattactgtcagcagtaataaactagg 320  
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QY 247 GTTTATTACTGTACGACGCTAGCGACTGG 268  
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**RESULT**  
3



[illegible]

214	99tctggagacagactcactctccaccatcagcagactnagcctgaagatttccacatg	373
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300		

DEFINITION	EST178511 Pancreas tumor III Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain.
ACCESSION	A4367405
NID	g2019753
KEYWORDS	human.
SOURCE	Homo sapiens
ORGANISM	Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.
REFERENCE	1 (bases 1 to 363)

Moreno-Palmaroux, P. F., McDonald, L. A., Nguyen, D. T., Pelligrino, P. H., Phillips, C. A., Pyder, S. F., Scott, L., Sandek, D. M., Shirley, R., Small, K. V., Springs, J. A., Utterback, J. R., Weidman, J. F., Willy, L. Y., Zeman, R. J., and Zeman, W. J. 1995. The human gene for the  $\beta$ -subunit of the mitochondrial complex I NADH dehydrogenase (ND2) is located on chromosome 1p34.3. *Hum. Mol. Genet.* 4: 1031-1035.

Rednagel, D. P., Cao, L., Fardipae, A., Coleman, T. A., Collins, E., Dinko, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G. A., He, W. L., Hu, T. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., Hunglung, J., Li, H., Weissner, P. S., Olsen, R., Raymond, L., Wei, Y. F., Wang, T., Xu, C., Yu, G. L., Eichen, S. M., Millon, P. J., Fannon, M. F., Rosen, C. A., Haseltine, W. A., Fields, C. Fraser, C. M., and Venter, J. C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl.), 3-174 (1995)

96026280

JOURNAL  
MEDLINE

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Email: [arkerlavet@tigr.org](mailto:arkerlavet@tigr.org)  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human G



Index: chr1: 35353-35353: H. sapiens  
 Seq primer: M13 Reverse  
 Location/Qualifiers  
 1..353

## FEATURES

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/organism="Homo sapiens"  
 /note="Organ: pancreas; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 /clone\_lib="pancreas tumor III"  
 /dev\_stage="adult"  
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 Best Local Similarity 83.7%; Pred. No. 0.00e+00;  
 Matches 25; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
 Db 1 ctccagccacccctctgtctcctcaggggaagagtcacccctctcctcagggccagtc 60  
 QY 14 CTCAGCCACCCCTGTCTCTCTCAGGGGAAGAGTCACCCCTCTCTCTCAGGGCCAGTC 73  
 Db 61 agatgttggtacgtttcttctcctcaggtatcagcacaacccctggccaaacctccacgagctcc 120  
 QY 74 AGAGTGTTAACTAAGTACTTACCTGTACTCAACACAGAAAGCTGTCTCAGCTCTCCAGGCTCC 143  
 Db 121 tcatccatgggtgtctccacagggccactagctactccggccacacttcagtcggcggtgggt 180  
 QY 134 TCATCATGTATGTCATCCAGAGGCGCCAGTGGCTATCCATGATGATTCATGTTGAGTGGGT 193  
 Db 181 ctgacagagaattcactctcaccatccagcggcgtcagctgtgaggaacttggcactatct 240  
 QY 144 CTGACAGAGAATTCACTCTCACTCAACCAACCTAGAGGCTGGAAGATTTTGGCACTTATT 253  
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 QY 254 ACTGACACAGCGTAGCGACTGGG---TCACCTTGGGGGAGGAGCAAGAGTGGAGATCA 310  
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 QY 311 A 311

RESULT 7 AA360223 405 bp mRNA EST 21-APR-1997  
 LOCUS EST56944; lymph node II Homo sapiens cDNA 5' end similar to  
 DEFINITION similar to immunoglobulin kappa light chain, V region.  
 ACCESSION AA360223  
 NID G2012543  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotic; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
 Homo.  
 1 (bases 1 to 405)  
 AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,A.P., Fuldner,P.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,  
 Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fine,L.D.,  
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geohagen,N.S.,  
 Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Li,L.I., Marmaro,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Peilgrin,S.M.,  
 Phillips,C.A., Pyder,S.E., Scott,J.L., Sauder,D.M., Shirley,P.,  
 Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Wiley,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Kozak,M., Kuhlmann,H., Hungjun,J., Li,H., Meissner,P.S., Olson,H.,  
 Raymond,D., Wiley,P., Wing,J., Xu,C., Yu,C.L., Ruben,S.M.,  
 Dillion,P.J., Fannon,M.P., Posen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M., and Venter,J.C.

Initial assessment of human gene diversity and expression patterns

JOURNAL Nature 377 (6547 Suppl): 3-174 (1995)  
 MEDLINE 95026280  
 COMMENT

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 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/cgi-bin/hgi.cgi>)  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1..405

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 /note="Organ: lymph node; Vector: pBluescript SK-; Site\_1:  
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 /clone\_lib="lymph node I"  
 /dev\_stage="adult"  
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 Best Local Similarity 85.5%; Pred. No. 0.00e+00;  
 Matches 23; Conservative 0; Mismatches 23; Indels 3; Gaps 2;  
 Db 92 ctccagccacccctctgtctcctcaggggaagagtcacccctctcctcagggccagtc 151  
 QY 14 CTCAGCCACCCCTGTCTCTCTCAGGGGAAGAGTCACCCCTCTCTCTCAGGGCCAGTC 73  
 Db 152 agatgttggtacgtttcttctcctcaggtatcagcacaacccctggccaaacctccacgagctcc 211  
 QY 74 AGAGTGTTAACTAAGTACTTACCTGTACTCAACACAGAAAGCTGTCTCAGCTCTCCAGGCTCC 190  
 Db 212 tcatccatgggtgtctccacagggccactagctactccggccacacttcagtcggcggtgggt 271  
 QY 131 TCCTCATGTATGTCATCCAGAGGCGCCAGTGGCTATCCATGATGATTCATGTTGAGTGGGT 250  
 Db 272 ggtcttgagacacacttacttctcctcagggccactagctactcaggtcaggttcttgcatt 331  
 QY 141 GGTGTGGACAGATTCATCTCTCAGATTCATGATGATGATGATGATGATGATGATGATGATGAT 350  
 Db 332 attactatca 341  
 QY 251 ATTACTGTCA 260

RESULT 8 AA345485 403 bp mRNA EST 21-APR-1997  
 LOCUS EST51505; Gall bladder II Homo sapiens cDNA 5' end similar to  
 DEFINITION similar to immunoglobulin kappa light chain, V region (GB:X67673).  
 ACCESSION AA345485  
 NID G1997722  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotic; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
 Homo.  
 1 (bases 1 to 403)  
 AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,A.P., Fuldner,P.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,  
 Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fine,L.D.,  
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geohagen,N.S.,  
 Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Li,L.I., Marmaro,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Peilgrin,S.M.,  
 Phillips,C.A., Pyder,S.E., Scott,J.L., Sauder,D.M., Shirley,P.,  
 Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Wiley,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Kozak,M., Kuhlmann,H., Hungjun,J., Li,H., Meissner,P.S., Olson,H.,  
 Raymond,D., Wiley,P., Wing,J., Xu,C., Yu,C.L., Ruben,S.M.,  
 Dillion,P.J., Fannon,M.P., Posen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M., and Venter,J.C.

Initial assessment of human gene diversity and expression patterns





QY 195 T 195

RESULT 12  
 LOCUS AA295377 277 bp mRNA EST 18-APR-1997  
 DEFINITION EST100538 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.  
 ACCESSION AA295377  
 NID g1947711  
 KEYWORDS EST  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 277)  
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gockayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S., Gloeck, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Rydger, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Fertie, A., Fischer, J., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, T., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.F., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns  
 JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT Other ESTs: THCL69106  
 Contact: Kerlavage, AR  
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 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the tigr Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse

FEATURES  
 source  
 1..277  
 /organism="Homo sapiens"  
 /note="Organ: pancreas; Vector: pBluescript SK-; Site: 1-ECORI; Site 2: XhoI"  
 /clone\_lib="Pancreas tumor 1"  
 /dev\_stage="adult"  
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BASE COUNT 56 a 83 c 70 g 61 t 7 others

ORIGIN  
 Query Match 50.3%; Score 157; DB 24; Length 277;  
 Best Local Similarity 91.4%; Prod. No. 2,870,262;  
 Matches 191; Conservative 0; Mismatches 14; Indels 4; Gaps 3.

Db 70 accgagcttcagagaccctgtttgtntccaggagggaagaccacccctctcagg 129  
 QY 7 ACTGAGTCTTACGACACCTGTGTTTGTCTCCAGSGAAGAGGACCCCTCTCTGAGG 66  
 Matches 191; Conservative 0; Mismatches 14; Indels 4; Gaps 3.

Db 130 gccagtcagagtgattagcagcagctacttagcctggtaccagcaaaacccctggccagcgt 189  
 QY 67 GCCAGTCAGAGTCTTAACA--AG-TACTTAGCTGTGACACAGAACCTGGCCAGGCT 123

Db 190 ccagagntccatctatgttgatccagagaggccactggnatccacacaggttcagt 249  
 QY 124 CCCAGGCTCCTCATCTATGATGATCCCAAGAGGAGGACAGGATCCAGTCAGGTCAGT 184

Db 250 ggcagtggtctggagacag-cttcaactct 277  
 QY 184 GGCAGTGGGTCTGGACAGACTTCACTCT 212

RESULT 13  
 LOCUS AA327218 289 bp mRNA EST 20-APR-1997  
 DEFINITION EST30586 Colon 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VNI regions (GB:Z11894).  
 ACCESSION AA327218  
 NID g1979524  
 KEYWORDS EST  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 289)  
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gockayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S., Gloeck, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Rydger, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Fertie, A., Fischer, J., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, T., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.F., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns  
 JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the tigr Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse

FEATURES  
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 /note="Organ: colon; Vector: pBluescript SK-; Site: 1-ECORI; Site 2: XhoI"  
 /clone\_lib="Colon 1"  
 /dev\_stage="adult"  
 <1..>289

BASE COUNT 66 a 88 c 73 g 59 t 3 others

ORIGIN  
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 Best Local Similarity 90.4%; Prod. No. 4,040,258;  
 Matches 188; Conservative 0; Mismatches 17; Indels 3; Gaps 2.

Db 82 ctccagggaccctgtctgtntccagggaagaccacccctctcagagccagtc 141  
 QY 14 CTCACGACACCTGCTGTTTGTCTCCAGSGAAGAGGACCCCTCTCTGAGGTC 73



QY 67 GCCAGTCAGAGTGTAAACAAGTACTTAGCCTGCTGCTAGCAACAGAAAACTGGCCAGGCTGCC 126

Db 204 aggcctctcatctatgatgcatccaaacagggccactggca 243

|||||

QY 127 AGGCTCCTCATCTATGATGCATCCCAACAGGGCCACTGGCA 166

Search completed: Tue Feb 24 07:42:19 1998  
Job time : 173 secs.

\*\*\*\*\*  
W O R E A  
\*\*\*\*\*  
(TM)

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MPsearch\_n.a - n.a database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:34:25 1998 Maspar time 198 19 seconds  
818.703 Million cell updates/sec  
Tabular output not generated.

Title: SUS-08-844-215-16  
Description: (1-312) from USC08044215.seq  
Perfect Score: 312  
N.A. Sequence: 1 GAGTTCATCTACTCTCTAGC... GAGCAGAGGTGGAGATGAAA 312  
Comp: CTCAGATGAGTCTAGAGGCTG... CTCAGTTCATCTCTCTAGT

Scoring table: TABLE default  
Gap 5

Nmatch STD Dbase C. Query C

Searched: 555703 seqs 246912900 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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174-EST174 175-EST175 176-EST176 177-EST177 178-EST178

Statistics: Mean 9.906; Variance 1.931; scale 5.129

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Prod. No.
1	216	69.2	332	59	T29342	EST77491 Homo sapiens	0.000e+00
2	212	68.3	453	34	T29342	Y194309.1 Homo sapiens	0.000e+00
3	203	65.1	381	58	T29114	EST69430 Homo sapiens	0.000e+00
4	193	59.7	393	54	T29478	EST14997 Homo sapiens	0.000e+00
5	183	58.7	383	59	T29016	EST00071 Homo sapiens	0.000e+00
6	183	58.7	385	64	H26475	Y119065.1 Homo sapiens	0.000e+00
7	182	58.3	451	10	T29236	Y194309.1 Homo sapiens	0.000e+00
8	171	54.9	570	34	H27642	Y194309.1 Homo sapiens	4.430e-293
9	161	51.5	359	64	H27642	Y194309.1 Homo sapiens	4.430e-293
10	158	50.6	401	40	R10529	Y194309.1 Homo sapiens	8.360e-266
11	153	49.0	360	37	P29407	Y194309.1 Homo sapiens	2.320e-255
12	153	49.0	453	64	H44749	Y194309.1 Homo sapiens	2.320e-255
13	149	47.8	361	28	R51922	Y194309.1 Homo sapiens	5.050e-247
14	134	42.9	393	58	T27593	EST100653 Homo sapiens	5.470e-216
15	133	42.6	218	54	H27031	Y194309.1 Homo sapiens	7.760e-214
16	138	41.0	171	64	H25498	Y194309.1 Homo sapiens	1.590e-204
17	136	40.4	232	63	H25498	Y194309.1 Homo sapiens	2.070e-199
18	131	38.9	161	63	H25498	Y194309.1 Homo sapiens	2.070e-189
19	118	37.9	176	61	H24609	Y194309.1 Homo sapiens	2.360e-184
20	116	37.2	421	27	H48043	Y194309.1 Homo sapiens	5.390e-179
21	115	36.9	447	89	H70726	Y194309.1 Homo sapiens	7.010e-177
22	115	36.9	516	33	R67559	Y194309.1 Homo sapiens	7.010e-177
23	110	35.3	395	58	T29112	EST69384 Homo sapiens	1.090e-166
24	110	35.3	438	33	R64593	Y194309.1 Homo sapiens	1.090e-166
25	106	34.0	237	65	H29292	Y194309.1 Homo sapiens	1.360e-159
26	97	31.1	201	64	H26206	Y194309.1 Homo sapiens	1.860e-148
27	97	31.1	434	11	T29178	Y194309.1 Homo sapiens	1.860e-148
28	96	30.8	593	22	R28232	Y194309.1 Homo sapiens	1.860e-138
29	93	29.8	279	58	T29056	EST89211 Homo sapiens	1.850e-132
30	93	29.8	290	46	H25841	Y194309.1 Homo sapiens	1.850e-132
31	92	29.5	470	81	H29115	Y194309.1 Homo sapiens	1.930e-130
32	91	29.2	288	58	T27591	EST100107 Homo sapiens	1.790e-128
33	91	29.2	364	58	T27591	EST100107 Homo sapiens	1.790e-128
34	90	28.8	488	64	H25625	Y194309.1 Homo sapiens	1.790e-128
35	89	28.5	288	58	T27721	EST13441 Homo sapiens	1.790e-124
36	97	27.9	210	34	R69482	Y194309.1 Homo sapiens	1.590e-120
37	94	27.9	170	69	H44238	Y194309.1 Homo sapiens	1.590e-114
38	93	26.6	189	51	R29213	Y194309.1 Homo sapiens	1.590e-114
39	78	25.0	438	34	R25535	Y194309.1 Homo sapiens	7.020e-112
40	77	24.7	467	64	H27034	Y194309.1 Homo sapiens	7.020e-112
41	73	23.4	213	64	H25521	Y194309.1 Homo sapiens	6.840e-101
42	72	23.1	405	27	R49845	Y194309.1 Homo sapiens	3.930e-93
43	71	22.9	369	58	T27597	EST100475 Homo sapiens	2.940e-89
44	69	22.1	262	60	H44273	Y194309.1 Homo sapiens	1.950e-85
45	68	21.9	397	34	P29292	Y194309.1 Homo sapiens	1.950e-85

ALIGNMENTS

1 T29342 332 bp mRNA EST 06-SEP-1995  
LOCUS EST77491 Homo sapiens cDNA 5' end similar to immunoglobulin kappa  
DEFINITION light chain, V region (CB-M29469) (H13056).  
ACCESSION T29342  
NID G611440  
KEYWORDS EST  
SOURCE human primer-M13 Reverse 116317-Human FabryG35.







2

185 TASTTGGTGGTATGAGACTTCACTCTTCACTATTCAGCAAGCTACAGAGCTGCAAG-ATTT 242

Db 273 g

Db 273 gtggcagtggtcttgggacagacttcactttccatcatcaggagttaggcctaaattt 332

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QY 182 GTGGCACTGAGTGTGGAGAGATTCATCTTCACCATCATCAAGCTAGAGGCTGAGGATT 241
Db 333 ttgacctgtattactgt 349
QY 242 TTGCACTTTATTACTGT 258

RESULT 9
LOCUS H27642 359 bp mRNA EST 13-JUL-1995
DEFINITION Y161g07 r1 Homo sapiens cDNA clone 162780 5' similar to gb:X06764
ACCESSION H27642
NID 9897995
KEYWORDS EST.
SOURCE human clone=162780 library=Soares breast 3NBHBS vector=PT73D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13p1 Psitel-Not I Psitel-Eco RI Adult human
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified p773 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M. Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes,
Sarcopterygii; Chordata, Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 359)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, P., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 186
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
Source 1..359
Location/Qualifiers
/organism="Homo sapiens"
/clone="162780"

BASE COUNT 83 a 113 c 80 g 78 t 5 others
ORIGIN
Query Match 51.6% Score 161; DB 64; Length 359;
Best Local Similarity 87.3% Pred.No. 4,42e-272;
Matches 220; Conservative 3; Mismatches 26; Indels 6; Gaps 4,

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Db 147 agaatattgacacaccccttagctgtgtaccagcagaaacctggcagcctccagc 206
QY 74 AGAGTGTAAACAGT---ACTTAGCTGTGTACCAACAGAAACCTGGCCAGGCTCCAGGC 130
Db 207 tctctatctatcatcacacacagggctcactggcagccatccagacaggttcagtcagtcn 266
QY 131 TCTTCATCTATGATCATCCCAACAGAGGCTACTGGCATCCAGCCAGGTTTCAGTGGCAGTG 190
Db 267 ggtctgggacagacttttadtctaccatncaagtagactggagcctgaagattttcag 326

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QY 191 GGTCTGGGCAAGAGATTC-ACCTCTCAACCAT--CAGCAACCTAGAGAGCCT--TGAAGATTTTTTTT 247
Db 327 tatattactgtc 338
QY 248 TTTATTACTGTC 259

RESULT 10
LOCUS P10529 401 bp mRNA EST 06-APR-1995
DEFINITION Y131a06 r1 Homo sapiens cDNA clone 128434 5' similar to gb:X06764
ACCESSION R10529
NID 9762485
KEYWORDS EST.
SOURCE human clone=128434 library=Soares fetal liver spleen INELIS
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13p1 Psitel-Pac I Psitel-Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGGAAGAAATTAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified p773
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata, Vertebrata, Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini, Hominoidea, Homo.

REFERENCE 1 (bases 1 to 401)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, P., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 239
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
Source 1..401
Location/Qualifiers
/organism="Homo sapiens"
/clone="128434"

BASE COUNT 86 a 113 c 105 g 96 t 1 others
ORIGIN
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Best Local Similarity 91.6% Pred.No. 8,36e-266;
Matches 223; Conservative 0; Mismatches 11; Indels 10; Gaps 9;

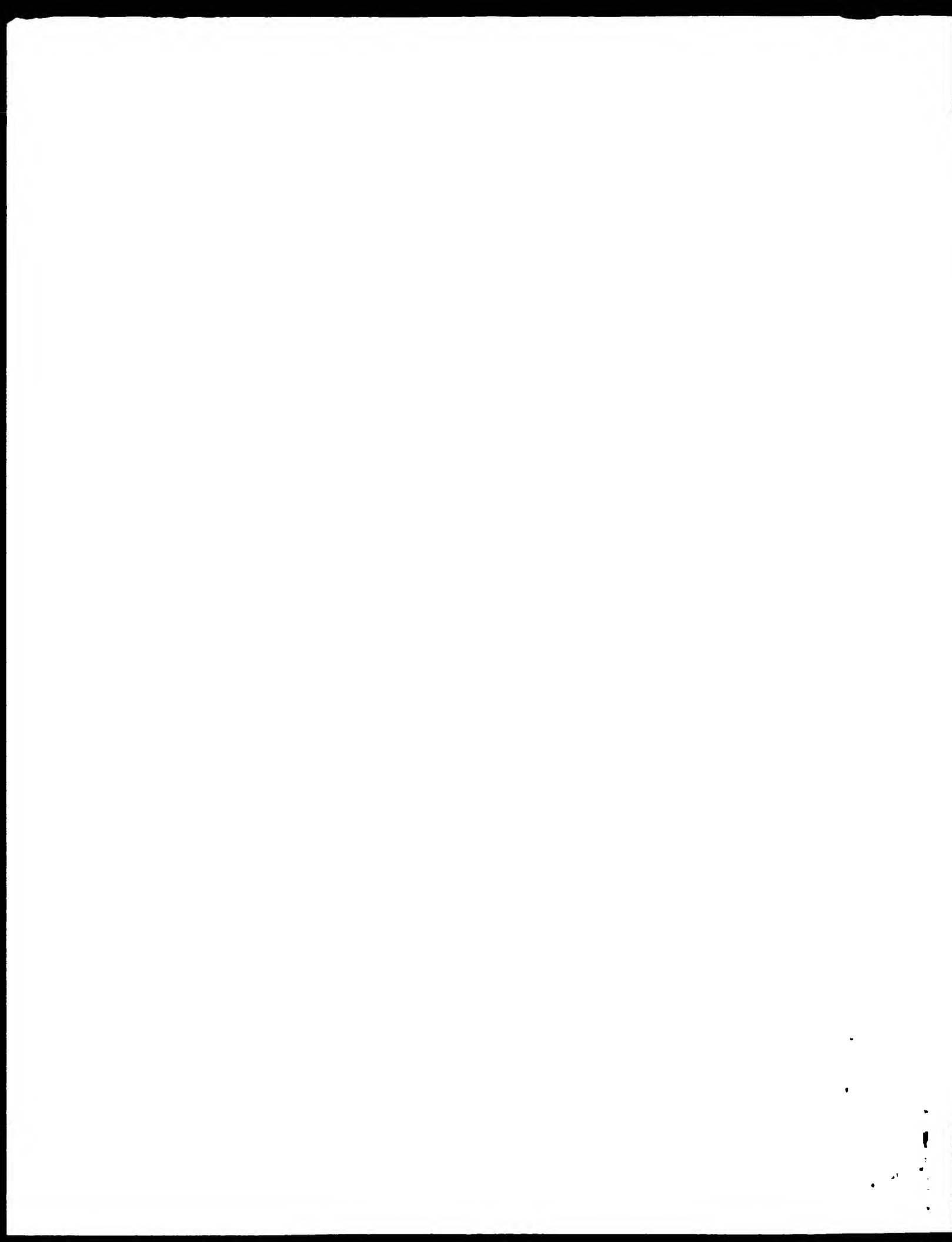
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Db 134 agaatattgacacaccccttagctgtgtaccagcagaaacctggcagcctccagc 193
QY 74 AGAGTGTAAACAGT---AG-TACTTAGCTGTGTACCAACAGAAACCTGG-CCAGGTTCAGG 124
Db 194 ctctctatctatgtgtgtcctcagcagggccactggcagcattcccccagacaggttcagtcagtc 253
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[illegible]

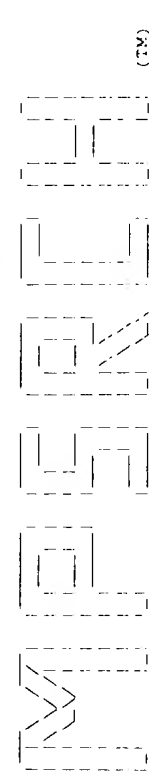








and is derived by analysis of the total score distribution.



\*\*\*\*\*  
Release 2.10 John F. Collins, Biocomputing Research Unit,  
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Distribution rights by IntelligentGenetics, Inc.  
\*\*\*\*\*  
MPsearch\_n a - a database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:23:13 1998, MasPar time 410.10 seconds  
Tabular output not generated  
1080.642 Million cell updates/sec  
Title: >US-08-844-215-16  
Description: (1-312) from "US08844215 seq  
Perfect Score: 312  
N A Sequence: 1 GAGTCATCTAGTCTTACG  
Comp: CTCGAGTGAGTCAGAGGTGG... GGCACCAAGTCAGATCAAA 312  
CTCGGTCACCTTGAATTT

Scoring table:  
Gap 5  
TABLE default  
Nmatch STD : Dbase 0: Query 0  
Searched: 430361 seqs, 710217276 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-new7  
1-BCT 2-FUN 3-GEN 4-HTG1 5-HTG2 6-HTG3 7-HTG4 8-HUM1  
9-HUM2 10-HUM3 11-INV1 12-INV2 13-ORG 14-MAM 15-VPT  
16-PLN 17-PPC1 18-PPC2 19-PPC3 20-SYN 21-UNC 22-VIP  
Database: genbank101  
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30-BCT8 31-BCT9 32-BCT10 33-BCT11 34-BCT12 35-BCT13  
36-GEN1 37-GEN2 38-GEN3 39-GEN4 40-GEN5 41-GEN6 42-HTG1  
43-HTG2 44-HTG3 45-HTG4 46-HTG5 47-INV1 48-INV2 49-INV3  
50-INV4 51-INV5 52-INV6 53-INV7 54-INV8 55-INV9 56-INV10  
57-INV11 58-INV12 59-MAM1 60-MAM2 61-MAM3 62-VPT1  
63-VPT2 64-VPT3 65-VPT4 66-PAT1 67-PAT2 68-PAT3 69-PAT4  
70-PAT5 71-PAT6 72-PAT7 73-PHG 74-PLN1 75-PLN2 76-PLN3  
77-PLN4 78-PLN5 79-PLN6 80-PLN7 81-PLN8 82-PLN9 83-PLN10  
84-PLN11 85-PLN12 86-PP11 87-PP12 88-PP13 89-PP14  
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108-PP123 109-PP124 110-PP125 111-PP126 112-STR 113-SYN  
114-UNA  
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Database: genbank-new7  
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132-VPT 133-PHG 134-PLN1 135-PLN2 136-PP11 137-PP12  
138-PP13 139-SYN 140-UNA 141-VRL  
Database: u-emb151\_101  
142-part1 143-part2

Database: genbank101  
115-VPL1 116-VPL2 117-VPL3 118-VPL4 119-VPL5 120-VPL6  
121-VPL7 122-VPL8 123-VPL9 124-VPL10 125-VPL11  
Database: genbank-new7  
126-BCT 127-GEN 128-HTG1 129-HTG2 130-INV 131-MAM  
132-VPT 133-PHG 134-PLN1 135-PLN2 136-PP11 137-PP12  
138-PP13 139-SYN 140-UNA 141-VRL  
Database: u-emb151\_101  
142-part1 143-part2  
Statistics: Mean 9.943; Variance 4.455; scale 2.232  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	278	89.1	324	98	HUMHEPB5AJ	Human hepatitis B sur	4,760,225
2	275	88.1	321	99	HUMIKCVH	Homo sapiens (clone F	2,560,224
3	274	87.8	321	99	HUMIKCVI	Homo sapiens (clone F	2,560,221
4	274	87.8	388	93	HSPOM604	H. sapiens mRNA for im	2,540,221
5	272	87.2	387	99	HUMICKVRG	Human immunoglobulin	1,970,219
6	268	85.9	381	91	HSIGVLLS	Human mRNA for LSI/VEV	1,980,215
7	266	85.3	333	91	HSAKD31G	H. sapiens rearranged	8,040,214
8	265	85.3	407	99	HUMIKKAX	Human Ig rearranged a	8,040,214
9	265	85.3	575	94	HSP03897	Human rheumatoid fact	8,040,214
10	265	84.9	384	93	HSPOM015	H. sapiens mRNA for im	5,920,213
11	264	84.6	242	93	HSSM044	H. sapiens mRNA for ka	5,950,212
12	264	84.6	345	93	HSSIP055	H. sapiens mRNA for ka	5,950,212
13	262	84.0	324	93	HUMIKKAMA	Homo sapiens anti-A m	1,450,210
14	260	81.3	294	93	HUMIKCRF	Homo sapiens (clone I	3,120,208
15	260	81.3	321	99	HUMIKCVC	Homo sapiens (clone P	3,120,208
16	260	81.3	321	99	HUMIKCVC	Homo sapiens (clone P	3,120,208
17	260	81.3	364	99	HUMAB49LG	Human mRNA for VL seq	3,120,208
18	259	81.0	297	93	HUMIKCCU	Homo sapiens (clone I	2,700,207
19	258	82.7	288	91	HSIGKV38	H. sapiens germline im	2,400,206
20	258	82.7	294	91	HSIGKV024	Human rearranged immu	2,400,206
21	258	82.7	321	93	HUMIKCVA	Homo sapiens (clone F	2,400,204
22	258	82.7	322	99	HUMIKCFDM	Homo sapiens (clone F	2,400,204
23	258	82.7	324	99	HUMIKCFD	Homo sapiens (clone F	2,400,204
24	258	82.7	345	93	HSSIP016	H. sapiens mRNA for ka	2,400,204
25	258	82.7	345	93	HSSIP026	H. sapiens mRNA for ka	2,400,204
26	258	82.7	364	99	HUMAB13LC	Human mRNA for VL seq	2,400,204
27	258	82.7	384	91	HSIGKLV68	H. sapiens mRNA for re	2,400,204
28	258	82.7	797	91	HSIGKLC1	Human germline frame	2,400,204
29	257	82.4	376	91	HSIGKLV33	H. sapiens mRNA for re	2,400,204
30	257	82.4	384	93	HSPOM023	H. sapiens mRNA for re	2,400,204
31	256	82.1	345	93	HSSIP042	H. sapiens mRNA for ka	1,770,204
32	256	82.1	345	93	HSSIP006	H. sapiens mRNA for ka	1,770,204
33	256	82.1	345	93	HSSIP017	H. sapiens mRNA for ka	1,770,204
34	256	82.1	387	93	HSPOM031	H. sapiens mRNA for im	1,770,204
35	256	82.1	797	99	HUMIKKVL	Human Ig germline Adj	1,770,204
36	254	81.4	321	99	HSPRIVL13	H. sapiens mRNA for re	1,300,202
37	254	81.4	323	99	HUMIKLRFH	Homo sapiens (HOLL) r	1,300,202
38	254	81.4	327	92	HSLKVL1	H. sapiens mRNA for re	1,300,202
39	254	81.4	333	95	HSP0772	Human anti-HIV-1 gp12	1,200,202
40	254	81.4	345	93	HSSIP011	H. sapiens mRNA for ka	1,300,202
41	254	81.4	345	93	HSSIP021	H. sapiens mRNA for ka	1,300,202
42	254	81.4	345	93	HSSIP022	H. sapiens mRNA for ka	1,300,202
43	254	81.4	345	93	HSSIP059	H. sapiens mRNA for ka	1,300,202
44	254	81.4	345	93	HSSIP020	H. sapiens mRNA for ka	1,300,202
45	254	81.4	345	93	HSSIP003	H. sapiens mRNA for ka	1,300,202

ALIGNMENTS

RESULT 1 HUMHEPB5AJ 324 bp mRNA PRI 17 JUN 1992  
LOC'S Human hepatitis B surface antigen antibody variable domain mRNA,  
DEFINITION partial cds.  
ACCESSION M83317  
NCI g183968  
KEYWORDS antibody variable domain; hepatitis B surface antigen antibody.  
SOURCE Homo sapiens (individual isolate JM, library: JM14, blood DNA to  
RNA.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 324)  
AUTHORS Zebec, S.T., Barbas, C.F. III, Henry, M.L., Cauchon, P., Graft, R.,  
DeGraw, J., Pyati, J., Lapolla, P., Burton, D.R., Lerner, R.A. and  
Thornton, G.B.  
TITLE Human combinatorial antibody libraries to hepatitis B surface

JOURNAL antigen  
MEDLINE Proc Natl Acad Sci U S A 89, 3175-3176 (1992)  
FEATURES 92228746

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CDS  
BASE COUNT 73 a 100 c 83 g 58 t

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Best Local Similarity 96.5%; Pred. No. 4.76e-225;  
Matches 304; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

Db 4 gqgctcagcagctcctccagccacccctgtcttctccagggaagagccacccctcc 63  
Qy 1 GAGCTCAGCTCTCCAGCCACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCC 60  
Db 64 tgcaggccagtcagagtgtagcagctactttagcttaccacagaaacctggccag 123  
Qy 61 TGCAGGGCCAGTCAGAGTGTTAAAGTACTTAGCCCTGGTACCAGCAACACCTGGCCAG 120  
Db 124 gctccagcctcctcatatgatcatcacaagagccactggcctccagccaggttc 183  
Qy 121 GCTCCAGGCTCTCTCATATGATGATCAATCAACAGSGGCTACTGGCATCCCGCAGGCTC 180  
Db 184 agtggcagtggtctgggacagacttccactctcaccatcagcagcctgaagat 243  
Qy 181 AGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCTGAAGAT 240  
Db 244 ttgcagtttattactgtcagcagcgttagcaactggcctcctctcttccggcgaggacc 303  
Qy 241 TTGCAGTATTATTACTGTACAGCGTATGCGACTGGG-TCA--CTTTGGCGGAGGAGCC 297  
Db 304 aaggtggagatcaaa 318  
Qy 298 AAGGTGGAGATCAAA 312

RESULT 2 HUMIKCVH 321 bp mRNA PRI 02-MAY-1996  
LOCUS Homo sapiens (clone pAG21) Ig kappa chain mRNA, V-region, partial cds.  
DEFINITION L37308  
NID g845531  
KEYWORDS immunoglobulin light chain; kappa-immunoglobulin; variable region.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Chlin.M., Sundqvist.V.A., Mach.M., Wahren.B. and Borrebaeck.C.A.  
TITLE Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus gp58/116 (gB), as determined with human monoclonal antibodies  
J. Virol. 67 (2), 703-710 (1993)  
JOURNAL 93124562  
MEDLINE  
REFERENCE 2 (bases 1 to 321)  
AUTHORS Chlin.M., Gwan.H., Mach.M. and Borrebaeck.C.A.  
TITLE Light chain shuffling of a high affinity antibody results in a drift in epitope recognition  
Mol. Immunol. 33 (1), 47-56 (1996)  
JOURNAL 96174997  
MEDLINE

FEATURES Location/Qualifiers  
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/clone="pAG21"  
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/product="immunoglobulin kappa-chain V3a region"  
misc\_difference 1..321  
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BASE COUNT 75 a 98 c 81 g 67 t

ORIGIN  
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Best Local Similarity 96.2%; Pred. No. 3.06e-222;  
Matches 302; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

Db 8 agatgaccagctccagccacccctgtcttctccagggaagagccacccctcc 67  
Qy 2 AGCTCATCTAGTCTCCAGCCACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCC 61  
Db 68 gcaggccagtcagagtgtagcagctactttagcttaccacagaaacctggcag 127  
Qy 62 GCAGGGCCAGTCAGAGTGTTAAAGTACTTAGCCCTGGTACCAGCAACCTGGCCAG 121  
Db 128 ctccagcctcctcatatgatcatcacaagagccactggcctccagccaggttc 187  
Qy 122 CTCGCCAGCTCTCTCATATGATGATCAATCAACAGSGGCTACTGGTATCCAGGTCA 181  
Db 188 gtggcagtggtctgggacagacttccactctcaccatcagcagcctgaagat 247  
Qy 182 GTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCTGAAGAT 241  
Db 248 ttgcagtttattactgtcagcagcgttagcaactggcctcctccttccggcgaggacca 307  
Qy 242 TTGCAGTATTATTACTGTACAGCGTATGCGACTGGG---TCACTTGGCGGAGGAGCA 298  
Db 308 aggtggagatcaaa 321  
Qy 299 AGGTGGAGATCAAA 312

RESULT 3 HUMIKCVI 321 bp mRNA PRI 02-MAY-1996  
LOCUS Homo sapiens (clone pAG21B) Ig kappa chain mRNA, V-region, partial cds.  
DEFINITION L37309  
NID g845533  
KEYWORDS immunoglobulin light chain; kappa-immunoglobulin; variable region.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Chlin.M., Sundqvist.V.A., Mach.M. and Borrebaeck.C.A.  
TITLE Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus gp58/116 (gB), as determined with human monoclonal antibodies  
J. Virol. 67 (2), 703-710 (1993)  
JOURNAL



Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 387)  
 AUTHORS Ploix, J. D., Zdzarsky, E., Newkirk, M. M. and Pauch, J.  
 TITLE Anti-DNA and anti-platelet specificities of SLE-derived autoantibodies: evidence for CD24H mutations and CDR3H motifs Mol. Immunol. 32 (10), 683-696 (1995)

JOURNAL 95388068  
 MEDLINE  
 REFERENCE 2 (bases 1 to 387)  
 AUTHORS Pauch, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-NOV-1994) Joyce Pauch, Montreal General Hospital Research Institute, McGill University, Rheumatology, Montreal, Quebec, H3G 1A4, Canada

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 322..324  
 /gene="IGKV"  
 /note="G00-119-341; putative"  
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 325..363  
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 364..387  
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BASE COUNT

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 Matches 298; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

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 Qy 7 ACTCAATCTCCAGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 66  
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Db 112 gccagtcagagtggttagcagctacttagctgtatccacacacacacacacacacac 171  
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 Qy 67 GCCAGTCAAGAGTGTAAACAAGTACITAGCCIGGTACACACAGAAACCTGGCAGG 126  
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Db 172 aggtctctcatatgatgcattccacacagggccactggcattccacacacacacacac 231  
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 Qy 127 AGGTCTCTCATATGATGATGATCAACAGGGGCTCACTGTCATCCAGGCTTCAGTGG 186  
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Db 232 agtggctctggacagacacttcactctcaccatccacagcctagaccccaagatttcc 291  
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 Qy 187 AGTGGGCTCTGGACAGACACTTCACCTCACCATCAGCAACCTAGACCTCTCAACAT 246  
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Db 292 gttattactgtcagcagcgtagcaactgggtgctcactttcggggagggagcagggg 351  
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 Qy 247 GTTTATTACTGTGACGAGGCTAGTGTACTGSSGT---ACTTTGAGGAGAGGAGAGG 303  
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Db 352 gagatcaaaa 360  
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 Qy 304 GAGATCAAA 312

RESULT 6  
 LOCUS H5IGVLLS 381 bp RNA PRI 31-MAR-1995  
 DEFINITION Human mRNA for LSI/EVB Ig V(kappa), autoantibody with RBC specificity.  
 ACCESSION X15987 Y00652  
 NID g33756  
 KEYWORDS Ig D-segment; Ig kappa light chain; Ig light chain; immunoglobulin joining region; variable region.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 381)  
 AUTHORS Silberstein, L.E., Litwin, S. and Carmack, C.E.  
 TITLE Relationship of variable region genes expressed by a human B cell lymphoma secreting pathologic anti-Pr2 erythrocyte autoantibodies J. Exp. Med. 169 (5), 1631-1643 (1989)

JOURNAL 89233583  
 MEDLINE  
 REFERENCE 2 (bases 1 to 381)  
 AUTHORS Carmack, C.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUL-1989) to the EMBL/GenBank/DBJ databases

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 346..381  
 /note="J(kappa) segment"

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Best Local Similarity 95.8%   Pred. No. 1.08e-215;
Matches 296; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

Db 73 acacagctctcagccacccctgtttgtctccaggggaaagagccactctctctcaggg 132
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QY 7 ACTCACTCTCCAGCCACCCCTGTCTTGTCTCCAGGGGAAAGAGCCACTCTCTCTGCAAG 66
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Db 133 gccagtcacagtgcttagcagctacttagctgtgtaccacacagacgctggccagctccc 192
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QY 67 GCACAGTCAGAGTGTTAACAGAGTACTTAGCTGTGTACCCACACACAAACCTGGCCGCTCCC 126
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Db 193 aggtctctctatgatcatcatcaacagggccactggcattcccccagcaggttcagtgcc 252
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QY 127 AGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186
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Db 253 aaggtctctcaggaatttcaactctcaccatcacagcagcctagagcctgaagattttcag 312
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QY 197 AGTGGGTCTGGACAGACTTCTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 246
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QY 247 GTTAACTCTCAGCAGCGTAACTGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 303
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QY 304 GAGATCAAA 312

RESULT 7 HSKA3DLIG 333 bp PNA PRI 10-JUN-1992
LOCUS H.sapiens rearranged Humiqa3dl gene encoding IgG light chain.
ACCESSION X59705
NID 934022
KEYWORDS IgG; immunoglobulin; J-segment; light chain.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 333)
AUTHORS Giese, T., Lu, E. W., Huang, D. F., Soto-Gil, P. W., Leffler, M., Kozin, F., Carson, D. A., and Chen, P. P.
TITLE Genetic analysis of self-associating immunoglobulin G rheumatoid factors from two rheumatoid synovia implicates an antigen-driven response
JOURNAL J. Exp. Med. 175 (3), 831-842 (1992)
MEDLINE 92156804
REFERENCE 2 (bases 1 to 333)
AUTHORS Tsalwei, Q.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-1992) Q. Tsalwei, Department of Medicine - 0563, University of California, San Diego La Jolla, California 92093-0663, USA

FEATURES             location/Qualifiers
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Matches 295;  Conservative 0;  Mismatches 11;  Indels 3;  Gaps 1;

Db 96 acacagtctccagacacccctgttctctccagggaaagagccacccctctctctcaggg 155
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Db 156 gccactcagagttagcaactacttagcctagctagtcacacacacacacacacacaccc 215
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Qy 67 GCCAGTCAGAGTGTATCAAGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCC 126

Db 215 aggtctctctctatgatgcacacacacacacacacacacacacacacacacacacacac 275
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Qy 127 AGGCTCTCTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186

Db 276 agtggtctctggacagacttctctcaccatcagcagcagcagcagcagcagcagcagcagc 335
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Qy 187 AGTGGGCTCTGGACAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246

Db 336 gtttattactgtcagcagagtagcaagtgtcctctcacttctcggcgagggacacaggtg 395
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Qy 247 GTTATTACTGTCTAGAGCTAGAGCTAGAGCTAGAGCTAGAGCTAGAGCTAGAGCTAGAG 303

Db 396 gagatcaaa 404
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Qy 304 GAGATCAAA 312

RESULT 9
LOCUS HSU03897 675 bp DNA PRI 02-AUG-1994
DEFINITION Human rheumatoid factor D1 IgG light chain VK3 region rearranged
           (humka3d1) gene, partial cds.
ACCESSION U03897
NID 9485725
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE Deftos, M., Olee, T., Carson, D.A. and Chen, P.P.
DEFINING the genetic origins of three rheumatoid synovium-derived
IgG rheumatoid factors
J. Clin. Invest. 93 (6), 2545-2553 (1994)
MEDLINE 94259815
REFERENCE 2 (bases 1 to 675)
AUTHORS Chen, P.P.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1993) Popen V. Chen, Medicine, University of
California San Diego, 9500 Gilman Dr., La Jolla, CA 92093-0663, USA
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Matches 295;  Conservative 0;  Mismatches 11;  Indels 3;  Gaps 2;

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RESULT 10
LOCUS HSPOM015 384 bp DNA PRI 02-JUN-1996
DEFINITION H sapiens mRNA for immunoglobulin kappa light chain VJ region (H
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ACCESSION Z68991
NID 91359843
KEYWORDS immunoglobulin; immunoglobulin kappa chain; immunoglobulin light
SOURCE chain; joining region; variable region.
ORGANISM human.
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE Juul, L., Hougs, L., Andersen, V., Sveigaard, A. and Parington, T.
DEFINING the genetic origins of three rheumatoid synovium-derived
IgG rheumatoid factors
J. Clin. Invest. 93 (6), 2545-2553 (1994)
MEDLINE 94259815
REFERENCE 2 (bases 1 to 384)
AUTHORS Juul, L.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1996) Juul L., Dept. of Clinical Immunology FI
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
2200 Copenhagen N, DENMARK

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Best Local Similarity 94.5% Pred No 3,25e-208;
Matches 277 Conservative 0 Mismatches 17 Indels 3 Gaps 0
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RESULT 15
LOCUS HUMKOVE 321 bp mRNA PRI 02-MAY-1996
DEFINITION Homo sapiens (clone PAC33, PAC36) Ig kappa chain mRNA, V-region, partial cds.
ACCESSION L37105
NID Q845525
KEYWORDS immunoglobulin light chain; kappa-immunoglobulin; variable region
SOURCE Homo sapiens (clone PAC33) cDNA to mRNA; and Homo sapiens (clone PAC36) cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Chin.M., Sundqvist.V.A., Mach,M., Wahren.B. and Borrebaeck,C.A.
TITLE Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus gp58/116 (gp), as determined with human monoclonal antibodies
JOURNAL J. Virol. 67 (2), 703-710 (1993)
MEDLINE 93124562
REFERENCE 2 (bases 1 to 321)
AUTHORS Chin.M., Owan.H., Mach,M. and Borrebaeck,C.A.
TITLE Light chain shuffling of a high affinity antibody results in a drift in epitope recognition
JOURNAL Mol. Immunol. 33 (1), 47-56 (1996)
MEDLINE 96174997
FEATURES
Location/Qualifiers
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11

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WILEY  
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(TM)

Release 2.1D John F. Collins, Bioinformatics Research Unit.  
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.  
Distribution rights by IntelliGenetics, Inc.  
  
MPSrch\_nu n a - n a database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 13:56:38 1998. MasPar time 19.34 seconds  
Tabular output not generated. 742.038 Million cell updates/sec  
  
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Comp: CTCGAGTGAGTACAGAGGTCG.....GACCAAGGTCAGATCAAA 312

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Searched: 87531 seqs, 22996021 bases x 2  
  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
  
Database: n-issued  
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Statistics: Mean 7.621; Variance 4.215; scale 1.808  
  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	252	80.8	900	7	US-08-053-	Sequence 180, Applicat	6.69e-169
3	228	73.1	646	13	PCR-US95-1	Sequence 2, Applicatio	1.30e-150
4	228	73.1	646	13	PCR-US94-0	Sequence 2, Applicatio	1.30e-150
5	228	73.1	646	7	US-08-300-	Sequence 2, Applicatio	1.30e-150
6	218	69.9	900	7	US-08-053-	Sequence 182, Applicat	5.22e-143
7	206	66.0	325	11	PCR-US93-1	Sequence 1, Applicatio	6.70e-134
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9	162	51.9	729	13	PCR-US95-0	Sequence 152, Applicat	1.10e-100
10	162	51.9	729	13	PCR-US95-0	Sequence 152, Applicat	1.10e-100
11	162	51.9	729	13	PCR-US95-0	Sequence 152, Applicat	1.10e-100
12	162	51.9	13254	13	US-08-376-	Sequence 156, Applicat	1.10e-100
13	162	51.9	13254	13	PCR-US95-0	Sequence 156, Applicat	1.10e-100
14	162	51.9	13254	13	PCR-US95-0	Sequence 156, Applicat	1.10e-100
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43 123 39.4 318 11 PCR-US93-0 Sequence 3, Applicatio  
44 123 39.4 318 11 PCR-US93-0 Sequence 3, Applicatio  
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ALIGNMENTS

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ID US-08-053-131-178 STANDARD: DNA; UNC: 812 BP.  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 178, Application US/08053131.  
CC Sequence 178, Application US/08053131  
CC Patent No. 5661016  
CC GENERAL INFORMATION:  
CC APPLICANT: Lonberg, Nils  
CC APPLICANT: Kay, Robert M.  
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
CC TITLE OF INVENTION: Producing Heterologous Antipodies  
CC NUMBER OF SEQUENCES: 197  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Townsend and Townsend Kourie and Crew  
CC STREET: One Market Plaza, Stewart Tower, Suite 200  
CC CITY: San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94105  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patented Release #1.0. Version #1.25  
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CC APPLICATION NUMBER: US/08/053/131  
CC FILING DATE: 26-APR-1993  
CC CLASSIFICATION: 800  
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CC APPLICATION NUMBER: US 07/000,860  
CC FILING DATE: 15-DEC-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/950,279  
CC FILING DATE: 17-DEC-1991  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/853,408  
CC FILING DATE: 18-MAR-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 14643-9-3  
CC TELECOMMUNICATION INFORMATION:





CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Scripps Research Institute  
 CC STREET: 10556 No 5667988th Torrey Pines Road, TPCR  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent in Release #1.0, Version #1.25  
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 CC FILING DATE: 02-SEP-1994  
 CC CLASSIFICATION: 435  
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 CC APPLICATION NUMBER: US 08/174,674  
 CC FILING DATE: 28-DEC-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/826,623  
 CC FILING DATE: 27-JAN-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/012,566  
 CC FILING DATE: 02-FER-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO. 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 646 base pairs  
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 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: cDNA  
 CC HYPOTHETICAL: NO  
 CC ANTI-SENSE: NO  
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 DT 01-JAN-1900  
 DE Sequence 182, Application US/08053131.  
 CC Sequence 182, Application US/08053131  
 CC Patent No. 5661016  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Lonberg, Nils  
 CC APPLICANT: Kay, Robert M.  
 CC TITLE OF INVENTION: Transgenic No 5661016-Human Animals for  
 CC TITLE OF INVENTION: Producing Heterologous Antibodies  
 CC NUMBER OF SEQUENCES: 197  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew  
 CC STREET: One Market Plaza, Stewart Tower, Suite 200  
 CC CITY: San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94105  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
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 CC APPLICATION NUMBER: US/08/053,131  
 CC FILING DATE: 26-APR-1993  
 CC CLASSIFICATION: 800  
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 CC APPLICATION NUMBER: US 07/990,860  
 CC FILING DATE: 16-DEC-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/810,274  
 CC FILING DATE: 17-DEC-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/853,408  
 CC FILING DATE: 18-MAR-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Smith, William M.  
 CC REGISTRATION NUMBER: 30,223  
 CC REFERENCE/DOCKET NUMBER: 14643-9-3  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415-326-2400  
 CC TELEFAX: 415-326-2422  
 CC INFORMATION FOR SEQ ID NO 182:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 900 base pairs  
 CC TYPE: nucleic acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: DNA (genomic)  
 CC FEATURE:  
 CC NAME/KEY: CDS  
 CC LOCATION: join(116..163, 351..650)  
 CC Sequence 900 BP; 220 A; 241 C; 201 G; 238 T; 0 other;  
 Query Match 69.9%; Score 218; DB 7; Length 900;  
 Best Local Similarity 94.6%; Pred No 5 (2e-143);  
 Matches 247; Conservative 0; Mismatches 11; Indels 3; Gaps 2;  
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 Db 455 GCGAGTCT 554







CC APPLICANT: Lerner, Richard A  
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Scripps Research Institute, Office of  
 CC ADDRESSEE: Patent Counsel  
 CC STREET: 10566 No. 56521st Torrey Pines Road, Suite 220,  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent Release #1 0, Version #1 25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCR1452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 155:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 729 base pairs  
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 CC STRANDEDNESS: double  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: DNA (genomic)  
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 Best Local Similarity 83.9% Pred. No. 1.10e-100  
 Matches 219 Conservative 0 Mismatches 36 Indels 3 Gaps 2

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RESULT 12  
 ID US-08-844-215-16 STANT-APC, INA, CNE, 13054 B6  
 AC XXXXX  
 DT 01-JAN-1998

DE Sequence 156, Application US/08276852.  
 CC Sequence 156, Application US/08276852.  
 CC Patent No. 5552138  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Burton, Dennis R  
 CC APPLICANT: Barbas, Carlos F  
 CC APPLICANT: Lerner, Richard A  
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Scripps Research Institute, Office of  
 CC ADDRESSEE: Patent Counsel  
 CC STREET: 10566 No. 56521st Torrey Pines Road, Suite 220,  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent Release #1 0, Version #1 25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
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 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCR1452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 156:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 13254 base pairs  
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 CC MOLECULE TYPE: DNA (genomic)  
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 Best Local Similarity 83.9% Pred. No. 1.10e-100  
 Matches 219 Conservative 0 Mismatches 36 Indels 3 Gaps 2

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 Cp 181 AGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1240  
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DT 01-JAN-1900  
DE Sequence 156, Application PC/TUS9508743.  
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CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1 25 (EPO)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/08743  
CC FILING DATE: 11-JUL-1995  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/276,852  
CC FILING DATE: 18-JUL-1994  
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CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 13254 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: circular  
CC MOLECULE TYPE: DNA (genomic)  
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Best Local Similarity 83.9%; Pred No 1.10e-100;  
Matches 219; Conservative 0; Mismatches 39; Indels 3; Gaps 2;  
Db 389 CTGACAGTAGTACAGTGCAGAACTTTTCAGGCTCCACTCTGCTGATGAGAGTGAAGTC 448  
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Db 449 TGTCCAGAGTACAGTGCAGAACTTTTCAGGCTCTAGGTTGTGATGCTGATGAGTGAAGTC 508  
Cp 201 TGTCCAGAGTACAGTGCAGAACTTTTCAGGCTCTAGGTTGTGATGCTGATGAGTGAAGTC 142  
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Cp 141 ATAGTATGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 85  
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Cp 84 GTTACAGTCTGAGTGCAGAACTTTTCAGGCTCTAGGTTGTGATGCTGATGAGTGAAGTC 25  
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DT 01-JAN-1900  
DE Sequence 170, Application US/08276852  
CC Sequence 170, Application US/08276852  
CC Patent No. 5652138  
CC GENERAL INFORMATION:  
CC APPLICANT: Burton, Dennis P  
CC APPLICANT: Barbas, Carlos F  
CC APPLICANT: Lerner, Richard A  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: The Scripps Research Institute, Office of  
CC ADDRESS: Patent Counsel  
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
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CC FILING DATE: 18-JUL-1994  
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DT 01-JAN-1900  
DE Sequence 170, Application PC/TUS9508743.  
CC Sequence 170, Application PC/TUS9508743  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS

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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SP91452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 170:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 13254 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: circular
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 13254 BP: 3238 A; 3251 C; 3559 G; 3206 T; 0 other;

Query Match      51.9%   Score 162; DB 7; Length 13254;
Best Local Similarity 83.9%   Pred. No. 1.10e-100;
Matches 219, Conservative 0, Mismatches 39, Indels 3, Gaps 2,

Db 389 CTGACAGTACTAGTCAAGTCTTCAGGCTCCACTCTGTGATGTTGAGAGTCAAGTC 448
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Search completed: Tue Feb 24 13:57:30 1998  
Job time : 52 secs.

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TITLE  
JOURNAL  
COMMENT

Martin, J., Moore, R., Schellenberg, K., Steptoe, M., Tan, F.,  
Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, P.  
WashU-NCI human EST Project  
Unpublished (1997)

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL: contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -28ml3 rev2 E1 from Amersham.

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strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
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M. Fatima Bonaldo."  
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NI Q2138915  
DT 01-JUN-1997 (Rel. 52, Created)  
DE 01-JUN-1997 (Rel. 52, Last updated, Version 1)  
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KW EST.  
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OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RP 1-269  
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,  
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,  
Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,  
White Y., Wylie T., Waterston R., Wilson P.;  
PA "WashU-Merck EST Project 1997";  
RL Unpublished.  
CC Contact: Wilson RK WashU-Merck EST Project Washington University  
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
CC est@watson.wustl.edu This clone is available royalty-free through  
CC LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for  
CC further information. Seq primer: -28ml3 rev2 E1 from Amersham.  
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FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a  
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strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],  
FT double-stranded cDNA was size selected, ligated to Eco RI  
FT adapters (Pharmacia), digested with Not I and cloned into  
FT the Not I and Eco RI sites of a modified pT73 vector  
FT (Pharmacia). Library constructed by Bento Soares and  
FT M. Fatima Bonaldo."  
FT /clone="770329"  
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RESULT 7  
ID AA476303 171 bp mRNA EST 19-MUN-1997  
DEFINITION 2W29D09.51 Soares ovary tumor NBHOT Homo sapiens cDNA clone 770705  
3' similar to gb:X6764 IG KAPPA CHAIN PREPUSOP V-III REGION  
(HUMAN).  
ACCESSION AA476303  
NID G2204514  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
Homo.  
REFERENCE 1 (bases 1 to 171)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.  
WashU-NCI human EST Project  
JOURNAL Unpublished (1997)





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        double-stranded cDNA was size selected, ligated to Eco RI
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        the Not I and Eco RI sites of a modified pT73 vector
        (Pharmacia). Library constructed by Bento Soares and
        M. Fatima Bonaldo."
        /clone="810346"
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      ACCESSION      AA494059
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      SOURCE      Homo.
      ORGANISM      Homo sapiens
        Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
        Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
        Homo.
      REFERENCE
        1 (bases 1 to 217)
        NCI-CGAP.
        National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
        Tumor Gene Index
        Unpublished (1997)
      JOURNAL
      COMMENT
        Contact: Robert Strausberg, Ph.D.
        Tel: (301) 496-1550
        Email: Robert_Strausberg@nih.gov
        Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael P.
        Emmert-Buck, M.D., Ph.D.
        cDNA Library Preparation: David B. Krizman, Ph.D.
        DNA Sequencing by: Greg Lennon, Ph.D.
        DNA Sequencing by: Washington University Genome Sequencing Center
        Clone distribution: NCI-CGAP clone distribution information can be
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        www-bio.llnl.gov/bbrp/image/image.html
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          modified polylinker; Site1: Not I; Site2: Eco RI; 1st
          strand cDNA was primed with a Not I - oligo(dT) primer [5'
          TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
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          the Not I and Eco RI sites of a modified pT73 vector
          (Pharmacia). Library constructed by Bento Soares and
          M. Fatima Bonaldo."
          /clone="810346"
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          /sex="female"
          /tissue_type="ovarian tumor"
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          /db_xref="GDB:6040648"
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          Best Local Similarity 92.9%; Pred. No. 4.34e-251;
          Matches 196; Conservative 0; Mismatches 10; Indels 5; Gaps 3;
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        NI      92189108
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        OS      Homo sapiens (human)
        OC      Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
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        RN      [1]
        RP      1..324
        RA      Hillier L., Allen M., Bowles L., Dubuque T., Geisels C., Jost S.,
        RA      Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
        RA      Moore B., Schellenberg K., Steptoe M., Tan F., Theising R.,
        RA      White Y., Wylie T., Waterston R., Willson R.:
        RA      "WashU-Merck EST Project 1997";
        RL      Unpublished.
        CC      Contact: Willson RK WashU-Merck EST Project Washington University
        CC      School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
        CC      MO 63108 Tel: 314 286 1820 Fax: 314 286 1810 Email:
        CC      est@wason.wustl.edu This clone is available royalty-free through
        CC      LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
        CC      further information. Seq primer: -28ml3 rev2 ET from Amersham High
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        FH      Key
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DT      23-FEB-1997 (Rel. 50, last updated; Version 5)
ET      26-FEB-1997 (Rel. 50, last updated; Version 5)
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DE      Q6711894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
KW      EST.
OS      Homo sapiens (human)

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OC	Vertebrate, mammalia, Eutheria, Primates, Catarrhini, Hominoidea.
CC	Homo.
CC	[1]
RN	1-360
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RA	NCI-CCAP;
RT	"National Cancer Institute, Cancer Genome Anatomy Project (CGAP)."
RI	Tumor Gene Index";
PL	Unpublished
CC	Contact: Robert Strausberg, Ph.D. Tel: (301) 426-1550 Email:
CC	Robert.Strausberg@nih.gov Tissue Procurement: W. Marston Linehan,
CC	M.D., Rodrigo Chagui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA
CC	Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed
CC	by Genome Systems Inc., Greg Lehoucq, Ph.D. DNA Sequencing by:
CC	Washington University Genome Sequencing Center Clone distribution:
CC	NCI-CCAP clone distribution information can be found through the
CC	I M A G F Consortium/LLNL at:
CC	<a href="http://www-bio.llnl.gov/dbfp/image/image.html">www-bio.llnl.gov/dbfp/image/image.html</a> Insert Length: 1066 Std
CC	Error: 0.00 seq primer: -41m13 fwd. Et from Amersham High quality
CC	sequence stop: 250.
CC	
CC	Location/Qualifiers
FF	Key

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/organism="Homo sapiens"
/clone="V201" /AMR10 Site1 Ncol Site2 EcoPst1 st
strand cDNA was primed with oligo(dT)17 on 50 ng of
RNAse-treated total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal prostate
epithelial cells. Double-stranded cDNA was ligated to EcoPst1
adaptors, 5 cycles of PCR applied to the cDNA with an
adaptor-specific primer, and the resulting PCR product
subcloned into pAMR10 by the ligation cloning method (Life
Technologies). Average insert size is 500 bp. NTE. Not
directly stored. This library was constructed by David
Krizman."
/cidenc="1009353"
/clone_lib="NCI_CGAP_Pri"
/sex="Male"
/dev_stage="45 years old"
/lab_host="Philip"

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FT  mRNA
SQ  Sequence 250 bp; 57 A; 84 C; 66 G; 49 T; 4 others;

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Best Local Similarity 92.2%; Pred. No. 333e-213;
Matches 154; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Db  90 cgcagctccaggccacctgttttctccagggaaggagccacctctctctgcagg 149
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QY  8 CGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCCCTCTCTGCA 67

Db  150 ccaatcagagtgcagcacagatacttagccctggtaccacacaaacccctgaccagct 209
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QY  68 CCAGTCCAGAGTGTACACAGCAATTAAGCTTGGTACCCAGAGACACTGATAGGTT 126

Db  210 cccaggtctctcatctatgctgcacccagggagggccactggtatccc 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  127 CCCAGGCTCTCATCTATGTTGTCATCCAGCAGGCGCCACTGGCATCCC 173

RESULT 14
LOCUS      AA225858      260 bp      mRNA      EST      20-JUN-1997
DEFINITION nc27d05.s1 NCI_CGAP_Prl Homo sapiens cDNA clone 3490 similar to
            gb:211894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION  AA225858
NID        91847166
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE  1 (bases 1 to 260)
AUTHORS   NCI-CGAP.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
            M.D., Michael Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1066 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 250.
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            /organism="Homo sapiens"
            /note="Vector: pAMP10; site.1: NotI; site.2: EcoRI; 1st
            strand cDNA was primed with oligo(dT)17 on 50 ng of
            DNase-treated, total cellular RNA obtained from
            5,000-10,000 microdissected, histologically normal
            prostate epithelial cells. Double-stranded cDNA was
            ligated to EcoRI adaptors, 5 cycles of PCR applied to the
            cDNA with an adaptor-specific primer, and the resulting
            PCR product subcloned into pAMP10 by the UDG-cloning
            method (Life Technologies). Average insert size is 500
            bp. NOTE: Not directionally cloned. This library was
            constructed by David Krizman."
            /clone_lib="NCI_CGAP_Prl"
            /sex="Male"
            /dev_stage="45 years old"
            /lab_host="DH10B"
            <1..260

Db  93 acgcagctccaggccacctgttttctccagggaaggagccacctctctgcagg 152
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    mRNA

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BASE COUNT      57 a      84 c      66 g      49 t      4 others
ORIGIN

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Query Match      43.1%; Score 137; DB 27; Length 260;
Best Local Similarity 92.2%; Pred. No. 333e-213;
Matches 154; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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Db  90 cgcagctccaggccacctgttttctccagggaaggagccacctctctctgcagg 149
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QY  8 CGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCCCTCTCTGCA 67

Db  150 ccaatcagagtgcagcacagatacttagccctggtaccacacaaacccctgaccagct 209
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QY  68 CCAGTCCAGAGTGTACACAGCAATTAAGCTTGGTACCCAGAGACACTGATAGGTT 126

Db  210 cccaggtctctcatctatgctgcacccagggagggccactggtatccc 256
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QY  127 CCCAGGCTCTCATCTATGTTGTCATCCAGCAGGCGCCACTGGCATCCC 173

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RESULT 15
LOCUS      AA492131      262 bp      mRNA      EST      10-JUL-1997
DEFINITION ng060902.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 939218 similar to
            gb:211894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION  AA492131
NID        92221693
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE  1 (bases 1 to 262)
AUTHORS   NCI-CGAP.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1015 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
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            /note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
            made by oligo-dT priming. Non- directionally cloned.
            Size-selected on agarose gel, average insert size 600 bp.
            Reference: Krizman et al. (1996) Cancer Research
            56:5380-5383."
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            /tissue_type="liposarcoma"
            /lab_host="DH10B"
            <1..262

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BASE COUNT      58 a      90 c      61 g      53 t
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Query Match      42.1%; Score 134; DB 38; Length 262;
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Matches 155; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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Db  93 acgcagctccaggccacctgttttctccagggaaggagccacctctctgcagg 152
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    mRNA

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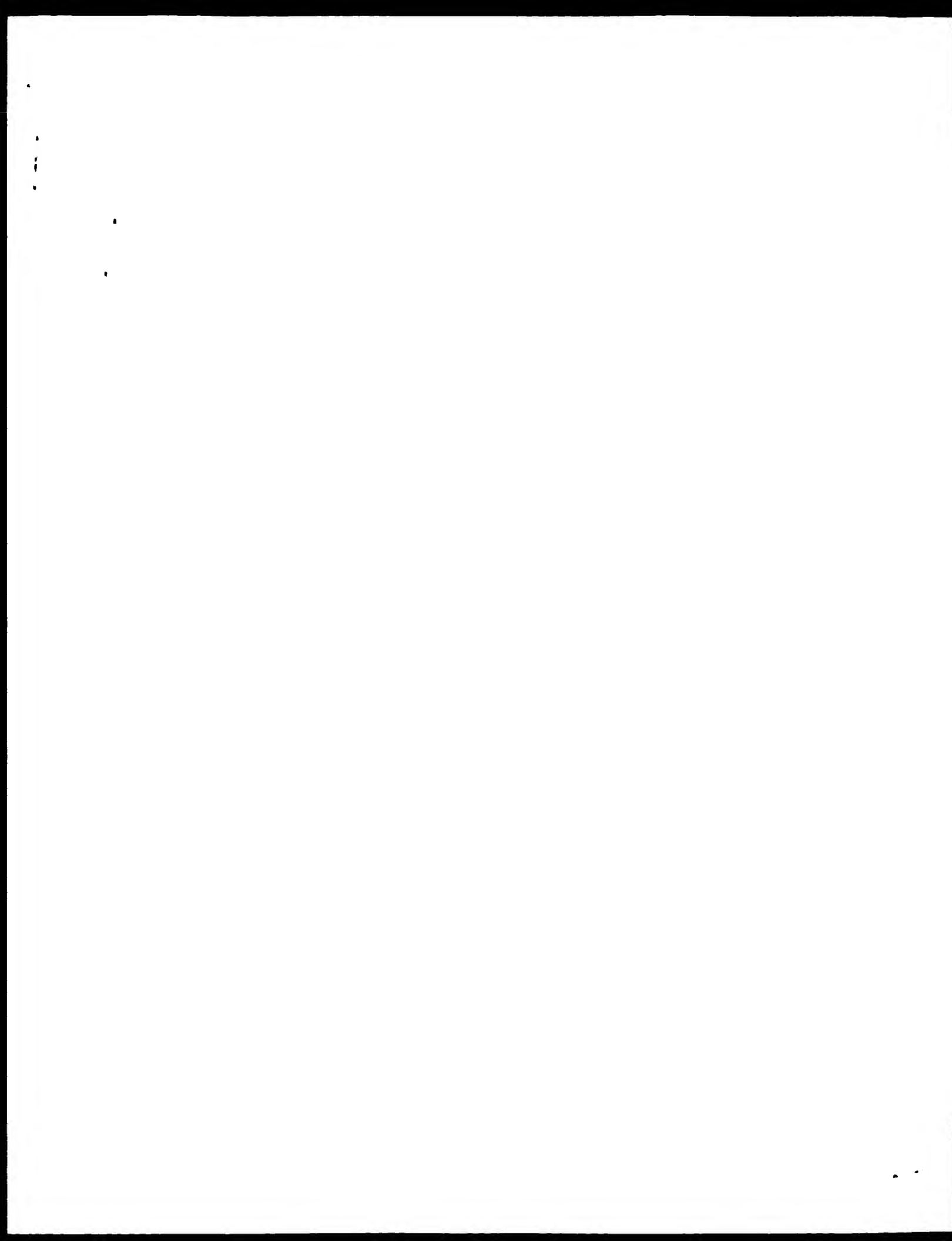
Thu Feb 26 07:04:10 1998

US-08-844-215-15.rstc

Page 9

Oy 7 ACGAGCTCCATGACGACGCTCTCTTTCTCTCTAGGAGGAAATAGGCAACCTCTCTCTTAGG 66  
 Db 153 GCCATCAGACGATGATGACGACAGCGCACTTAACTGTATACGACGACAAAGATGCGCAGCT 212  
 Oy 67 GGCATCTGAGATGTTATGACGACAACTTACTTACCTCTGGTACCGACGAGAACCTTGGCCAGGCT 126  
 Db 213 GCGAGATGCTCATCTATGATGATCGACGAGAGTGTGCACTGACATCCGACAG 262  
 Oy 127 GCGAAGGCTCTCATCTATGATGATGACGACGAGGCTCATCTGACATCCGACAGC 177

Search completed: Tue Feb 24 07:22:48 1998  
Job time : 170 secs.











Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /note="Organ: lymph node; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 /clone\_lib="Lymph node 1"  
 /dev\_stage="adult"  
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BASE COUNT 89 a 117 c 98 g 93 t 8 others

ORIGIN

Query Match 72.6%; Score 231; DB 52; Length 405;  
 Best Local Similarity 92.1%; Pred No 0.00e+00;  
 Matches 245; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 92 cctccaggcaccctgtcttctgtctctaggggaaacagccaccctctctgcaggcccaatc 151  
 QY 14 CTCACGGCACCCCTGTCCTTGTCTCTCCAGGGGAAAGAGAGCCACCTCTCTGCGAGGCTCAGTC 73

Db 152 agactgttagagacttctcttagcctgtaccagcagagaacacctggccaggctcccaaggc 211  
 QY 74 AGAGTGTATTAGTGTCA-GCTTTATGGTAACTCAAGT-TGACAGTGTGGGCAAGGG-ACC 303

Db 212 tctctctatctgtgtcaccagcaggggccactggccatcccccagacagcttccagtgaccatg 271  
 QY 134 TCCTCATCTATGCTGTCATCCAGCAGGGGCGCACTGGCACTCCAGACAGCTTAGTGGCACTG 194

Db 272 ggtcttgacanaacttnactntcancatcagcactggagcctggagcctgaacantttncatgt 331  
 QY 194 GGTCTGGACAGACACTTCACCTTCATCATCACTACAGCTGAGAGCTTTCAGATTCAGATTC 254

Db 332 attactgtcacttggtgtatggttagctca 357  
 QY 254 ATTACTGTGACGCTTTATGTGTAACATCA 279

RESULT 6  
 LOCUS AA295311 328 bp mRNA EST  
 DEFINITION EST100471 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.  
 ACCESSION AA295311  
 NID g1947646  
 KEYWORDS EST  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE 1 (bases 1 to 328)  
 AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Feldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geochagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Saudke,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Pannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 1-174 (1995)  
 MEDLINE 96026280  
 COMMENT Other ESTs: THC169106







QY 63 CAGGGCCAGCTCAGAGTGTAGCAGCAATTACTTAGCCTGGTACCAGCAGAGAGCTGGCCA 122  
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 QY 123 GGTCCAGAGGCTCTCTCATCTATGTGGTCATCCAGAGGAGGCTGCTGCTCAGCAGAGGTT 182  
 Db 251 cagtgcacgtggtgtgagacagacattccactctcaccat 289  
 QY 183 CAGTGGCACTGGTCTGGGACAGAGCTTCACCTCACCAT 221

RESULT 12  
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 DEFINITION EST100323 Pancreas tumor I Homo sapiens cDNA 5' end similar to  
 immunoglobulin kappa light chain, VJ regions.  
 ACCESSION AA295154  
 NID g1947509  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
 Homo.

REFERENCE 1 (bases 1 to 264)  
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A.,  
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,  
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,  
 Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,  
 Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Geoghagen, N.S.,  
 Glodak, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,  
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
 Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, P.,  
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Collins, E.J.,  
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
 Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,  
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,  
 Korzak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,  
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,  
 Dillion, P.J., Fannon, M.B., Rosen, C.A., Haseltine, W.A., Fields, C.,  
 Fraser, C.M., and Venter, J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280  
 Other\_ESTs: THC169106  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/html>)  
 Seq primer: M13 Reverse.

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 /clone\_lib="Pancreas tumor I"  
 /dev\_stage="adult"  
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 Best Local Similarity 94.1%; P-val No. 1 73e-247;  
 Matches 183; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 71 acgcagctccaggagccctgtnttctgtctccaggggaagagccaccctctctcaggg 130

QY 7 ACCGAGTCTCCAGGCACTGTCTTTGTCTCTAGAGGAAAGAGACACCTCTCTCTCTCT 66  
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 QY 67 GCCAGTCCAGAGTGTATGACCAATTAATAGCTGGTACGACAGAGACTGAGCTAGGCT 126  
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 QY 187 GGCAGTGGGCTGTG 200

RESULT 13  
 LOCUS AA366461 294 bp mRNA EST 21-APR-1997  
 DEFINITION EST177408 Pancreas tumor III Homo sapiens cDNA 5' end similar to  
 similar to immunoglobulin kappa light chain, V region.  
 ACCESSION AA366461  
 NID g2018779  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
 Homo.

REFERENCE 1 (bases 1 to 294)  
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A.,  
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,  
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,  
 Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,  
 Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Geoghagen, N.S.,  
 Glodak, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,  
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
 Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, P.,  
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Collins, E.J.,  
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 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,  
 Korzak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,  
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,  
 Dillion, P.J., Fannon, M.B., Rosen, C.A., Haseltine, W.A., Fields, C.,  
 Fraser, C.M., and Venter, J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280  
 Other\_ESTs: THC168243  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/html>)  
 Seq primer: M13 Reverse

FEATURES  
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 EcoRI: Site\_2: XhoI"  
 /clone\_lib="Pancreas tumor III"  
 /dev\_stage="adult"  
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 mpna  
 BASE COUNT 54 a 87 c 77 g 64 t 2 others  
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Best Local Similarity  98.2%   Prod No. 5,646-273:
Matches 168:  Conservative  0:  Mismatches  3:  Indels  0:  Gaps  0:

Ddb      99  accgagctccaggcacccctctctttgtctccagaggaagagacacccctctctccacag 154
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QY       7  AGCGASICTCCAGGACACCTCTCTTGTCTCCAGGGAAGAGACACCTCTCTCTCTCTCTCTCT 166
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Ddb     159  gccagctcagagtggttagcagcagctacctatccctggtagccagcagagacctggacagagc 214
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QY     67  GCCAGTCAGAGTGTTAGCAGCAATTACTTATGCTTGGTACCCAGCAGAGACACTTGGCCTASGCT 124

Ddb     219  cccagagctctctctatctatcggtgcattccacagcaggccactgcattcccaaac 269
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QY    127  CCCAGAGCTCTCTCATCTATGTTGCTATCGAGCAAGGCTACTGGCATCCAGAC 177

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DEFINITION	ES1/Y0963 1-cell lymphoma homo sapiens cDNA 3' end similar to similar to immunoglobulin kappa, variable region (GF:Y09649).
ACCESSION	AA361678
NID	G2013998
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 283) Adams,M.D., Kertavag,A.R., Fleischmann,P.D., Feldner,P.A., Eut,C.Y., Lee,N.H., Kirkness,E.F., Weisbach,K.S., Gayner,J.D., White,C., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.B., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geachagan,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,I.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanchares,F.F., McDonald,I.A., Nguyen,D.T., Pellingrino,S.M., Phillips,C.A., Pyder,S.E., Scott,T., Saudek,D.M., Shirley,R., Small,K.V., Springs,T.A., Utterback,T.P., Weidman,J., Wiley,

Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,  
 He, W., Hu, J. S., Green, M., Gruher, J., Hudson, P., Kim, A.K.,  
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P., Olsen, H.,  
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,  
 Dillion, P. J., Fannon, M. P., Rosen, C.A., Haseltine, W.A., Fields, C.,  
 Fraser, C.M., and Venter, J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (5547 Suppl.) 3-174 (1995)  
 95026380  
 Other ESTs: THC168243  
 Contact: Kerlavage, AR

Bioinformatics  
 The Institute for Genomic Research  
 3712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
     1..283  
         /organism="Homo sapiens"  
         /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
         XhoI"  
         /clone\_lib="T-cell lymphoma"  
         /cell\_type="T-lymphocyte"  
         -1..283  
             58 a      90 c      72 g      59 t      4 others  
 mpna  
 BASE COUNT



















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QY 127 CCCAGGCTCTCTATGTTGTCATCCAGCAGGCGCCACTGGCATCCCGACAGAGGTT-CAG 185
Db 250 tggcagtggtgtgagacagacttactcttcaccatcagcagcctagagccctgaaaga 309
QY 186 TGGAGAGTGGG-TCTGGGACAGAGATTTACTCT-CACCATAGAGAGACTGGAGGCTTGA-GA 242
Db 310 ttttgcaatttatta 324
QY 243 ITTTGAGTGTATTA 257

RESULT 13
LOCUS R44693 438 bp mRNA EST 26-MAY-1995
DEFINITION Y122799 r1 Homo sapiens cDNA clone 140009 5' similar to gb-M6343a
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION P44693
NID q836572
KEYWORDS EST.
SOURCE human clone-140009 library-Soares placenta Nb2HP vector-pT773D
(Pharmacia) with a modified polylinker host-BH10P (ampicillin
resistant) primer-M13P1 Rsite1-Not I Rsite2-Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5].
AACTGGAGAAATTCGGCCGACGAAATTTTTTTTTTTTTT 3', double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT773
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 438)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Pohlifing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson PK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 290
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information
FEATURES
source
Location/Qualifiers
1..438
/organism="Homo sapiens"
/clone="140009"
BASE COUNT 114 a 110 c 114 g 96 t 4 others
ORIGIN
Query Match 45.6% Score 145: DB 33: Length 438:
Best Local Similarity 92.6%: Pref No 1 56e-233:
Matches 163: Conservative 0: Mismatches 12: Indels 1: Gaps 1:
Db 1 atggtgcatccagagggccactgg-atccagacaggttccagcagtgaggtctggga 59
QY 143 ATGTGTATCCAGAGGAGGACCTGAGATGAGTACAGAGAGTGGTACAGTGGGAGTGGGGA 202
Db 60 cagacttcactctccacatcagcagagactgagcgtgaagattttgcagtgattactgtc 119
QY 203 CAGACTTCATCTCACCATTATGAGACTGGAGGCTTGAACATTTGGAGTGTATTTACTGTC 262
Db 120 agcaatatactctaccgtacacatttttggccagggggaccagctggagatcaaa 175

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QY 263 AGCTTTATGGTAACATCAGCTTGGACCTTGGCCCAAGGAGATCAGTGGATCAAA 318

RESULT 14
LOCUS R48043 421 bp mRNA EST 18-MAY-1995
DEFINITION YJ66e01.r1 Homo sapiens cDNA clone 153720 5' similar to gb-X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION R48043
NID q810069
KEYWORDS EST.
SOURCE human clone-153720 library-Soares breast 2NHRst vector-pT773D
(Pharmacia) with a modified polylinker host-BH10P (ampicillin
resistant) primer-M13P1 Rsite1-Not I Rsite2-Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5].
TGTACCAATTCAGTCTGGAGGAGGCGCCCTTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT773 vector (Pharmacia). Library went through one round
of normalization to a cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 421)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Pohlifing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson PK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 242
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information
FEATURES
source
Location/Qualifiers
1..421
/organism="Homo sapiens"
/clone="153720"
BASE COUNT 80 a 114 c 110 g 110 t 7 others
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Best Local Similarity 91.7%: Pref No 2 04e-325:
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Db 75 ctccagagaccctgtctgtctcagggagggagggagcaccctctctgacagccagtc 134
QY 14 CTCAGAGGACCCCTGTCTTGTCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 74
Db 135 agagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 194
QY 74 AGAGTGTAGCAGCAATTAATAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 134
Db 195 tctcatctatggtcattccaccagggcagcagcagcagcagcagcagcagcagcagcagcagc 254
QY 134 TCCTCATCTATGTCATCCAGCAGGGG-CCACTGGGCAT-CCACAGACAGGTT-CAGTGGG-C 189
Db 255 agtgaggtctngg 266
QY 190 AGTGGGCTCTGGG 201

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\*\*\*\*\*  
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\*\*\*\*\*  
MPSrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 13:44:51 1998. Master time 19.76 Seconds  
Tabular output not generated.  
Title: >US-08-844-215-15  
Description: (1-318) from US08844215.seq  
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N.A. Sequence: CCGAGTTCGAGTTCGAGG  
Comp: CCGAGTTCGAGTTCGAGG  
Scoring table: TABLE default  
Gap 6  
Nmatch STD : Dbase 0; Query 0  
Searched: 87521 seqs. 2294601 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: n-issued  
1 block1 2151 3152 4153 5154 6155 7156 8157 9158 10159  
10160 11161 12162 13163 14164 15165 16166 17167 18168 19169  
Statistics: Mean 7.613 Variance 4.275; scale 1.781  
pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.  
SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	272	85.5	325	11	PCT-US93-1 Sequence 1, Application	1,940-181
2	263	82.7	545	13	PCT-US95-1 Sequence 2, Application	1,160-174
3	263	82.7	545	12	PCT-US94-0 Sequence 2, Application	1,160-174
4	263	82.7	545	7	US-08-300-1 Sequence 2, Application	1,160-174
5	262	82.4	900	7	US-08-300-1 Sequence 182, Application	6,580-174
6	218	58.5	812	7	US-08-053-1 Sequence 178, Application	7,110-141
7	215	57.0	900	7	US-08-053-1 Sequence 190, Application	2,330-138
8	215	57.0	720	13	US-08-076-0 Sequence 172, Application	1,350-138
9	215	57.0	720	13	PCT-US94-0 Sequence 168, Application	1,350-138
10	215	57.0	720	13	US-08-076-0 Sequence 168, Application	1,350-138
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12	215	57.0	720	13	US-08-076-0 Sequence 168, Application	1,350-138
13	215	57.0	720	13	US-08-076-0 Sequence 168, Application	1,350-138
14	215	57.0	720	13	PCT-US94-0 Sequence 170, Application	1,350-138
15	215	57.0	720	13	US-08-076-0 Sequence 170, Application	1,350-138
16	142	44.7	397	5	US-08-017-1 Sequence 1, Application	2,010-84
17	141	44.3	350	5	US-08-026-1 Sequence 3, Application	1,110-83
18	135	42.5	329	11	PCT-US93-0 Sequence 7, Application	2,210-79
19	135	42.5	329	11	PCT-US93-0 Sequence 5, Application	2,810-79

20 130 40.9 321 7 US-08-425 Sequence 72, Application 1,290-76  
21 130 40.9 321 10 PCT-US92-0 Sequence 74, Application 1,290-76  
22 130 40.9 321 5 US-07-988 Sequence 74, Application 1,290-76  
23 130 40.9 321 7 US-08-425 Sequence 80, Application 1,290-76  
24 130 40.9 321 10 PCT-US92-0 Sequence 92, Application 1,290-76  
25 130 40.9 321 10 PCT-US92-0 Sequence 92, Application 1,290-76  
26 130 40.9 321 5 US-07-988 Sequence 92, Application 1,290-76  
27 130 40.9 321 5 US-07-988 Sequence 92, Application 1,290-76  
28 130 40.9 321 10 PCT-US92-0 Sequence 92, Application 1,290-76  
29 127 39.9 333 11 PCT-US93-0 Sequence 9, Application 2,020-73  
30 127 39.9 333 11 PCT-US93-0 Sequence 9, Application 2,020-73  
31 126 39.6 384 6 US-08-468 Sequence 13, Application 1,080-72  
32 126 39.6 384 6 US-08-259 Sequence 13, Application 1,080-72  
33 125 39.3 339 13 PCT-US95-1 Sequence 20, Application 5,830-72  
34 125 39.3 339 13 PCT-US95-1 Sequence 20, Application 5,830-72  
35 125 39.3 339 7 US-08-467 Sequence 50, Application 5,830-72  
36 125 39.3 5703 7 US-08-467 Sequence 50, Application 5,830-72  
37 125 39.3 5703 13 PCT-US95-1 Sequence 52, Application 5,830-72  
38 125 39.3 5703 7 US-08-470 Sequence 50, Application 5,830-72  
39 124 39.0 390 7 US-08-300-1 Sequence 62, Application 3,130-71  
40 124 39.0 390 13 PCT-US95-1 Sequence 62, Application 3,130-71  
41 124 39.0 321 10 PCT-US92-0 Sequence 71, Application 3,130-71  
42 124 39.0 321 5 US-07-988 Sequence 71, Application 3,130-71  
43 124 39.0 321 7 US-08-425 Sequence 69, Application 3,130-71  
44 124 39.0 449 1 US-08-020-4 Patent No. 5450303 3,130-71  
45 123 38.7 5238 1 US-08-363-1 Patent No. 5453363 1,680-70

ALIGNMENTS

RESULT 1  
ID PCT-US93-12501-1 STANDARD; DNA; UNC; 325 RP  
AC XXXXX  
DT 01-JAN-1900  
SE Sequence 1, Application PCT-US93-12501.  
CC Sequence 1, Application PCT-US93-12501  
CC GENERAL INFORMATION:  
CC APPLICANT: Chang, Tse Wen  
CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IGA MONOCLONAL ANTIBODIES AND  
CC TITLE OF INVENTION: RETAINED PROPERTIES FOR ALLERGY TREATMENT  
CC NUMBER OF SEQUENCES: 10  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Tanox Biosystems, Inc.  
CC STREET: 10301 Stella Link Rd.  
CC CITY: Houston  
CC STATE: Texas  
CC COUNTRY: USA  
CC ZIP: 77025  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3 5" Hi Density Diskette  
CC COMPUTED: IBM PS/2  
CC OPERATING SYSTEM: DOS, Version 3.30  
CC SOFTWARE: Wordperfect 5.1  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER PCT/US93/12501  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Mirabel, Eric P.  
CC REGISTRATION NUMBER: 31,211  
CC REFERENCE/DOCKET NUMBER: TXN92-3  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 713-664-2288  
CC TELEFAX: 713-664-8914  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 325 nucleotides  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double stranded  
CC TOPOLOGY: Linear

SQ Sequence 325 BP; 79 A; 93 C; 79 G; 74 T; 0 other;  
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Best Local Similarity 93.6%; Pred No. 1 94e-181;  
Matches 292; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 73 GCCAGTCAGACTGTAGCAGCAGACTAGCTGCTGGTACGAGCAGCAACTGGCCAGGCT 132  
QY 67 GCCAGTCAGACTGTAGCAGCAGACTAGCTGCTGGTACGAGCAGCAACTGGCCAGGCT 126  
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QY 127 CCCAGGCTCTCTATCTATCTGCTACATCAAGTCACTGCGCATCCCGACAGAGTTTCACT 186  
Db 193 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT 252  
QY 187 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT 246  
Db 253 GCAGTGTATTACTGTGACAGAGTTTGGTAACTCAGAGTGGAGGTTCCGGCCAGGACCAAG 312  
QY 247 GCAGTGTATTACTGTGACAGAGTTTGGTAACTCAGAGTGGAGGTTCCGGCCAGGACCAAG 306  
Db 313 GTTGAATCAAA 324  
QY 307 GTGAGATCAAA 318

RESULT 2  
ID PCT-US95-11235-2 STANDARD; DNA: UNC; 646 BP.  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 2, Application PC/TUS9511235.  
QY Sequence 2, Application PC/TUS9511235  
CC GENERAL INFORMATION:  
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIPOD LIBRARIES  
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS  
CC NUMBER OF SEQUENCES: 70  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: The Scripps Research Institute  
CC STREET: 10666 North Torrey Pines Road, TPC8  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1 0, Version #1 25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/11235  
CC FILING DATE: 01-SEP-1995  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/300,386  
CC FILING DATE: 02-SEP-1994  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/174,674  
CC FILING DATE: 28-DEC-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/826,623  
CC FILING DATE: 27-JAN-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/954,148  
CC FILING DATE: 30-SEP-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/012,566

CC FILING DATE: 02-FEB-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: TSP1 400 1 (PC)  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-554-2937  
CC TELEFAX: 619-554-6312  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 646 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA  
CC HYPOTHEICAL: NO  
CC ANTI-SENSE: NO  
SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;  
Query Match 82.7%; Score 263; DB 13; Length 646;  
Best Local Similarity 93.7%; Pred. No. 1 16e-174;  
Matches 298; Conservative 0; Mismatches 17; Indels 3; Gaps 1;

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QY 1 GAGCTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCAGCCCTCTCTCAGG 60  
Db 61 TGCAGGGGACGTCAGAGTGTAGCAGCAGACTTACTTATGCTGTTACGAGCAGAGTGTG 120  
QY 61 TGCAGGGGACGTCAGAGTGTAGCAGCAGACTTACTTATGCTGTTACGAGCAGAGTGTG 120  
Db 121 CAGGCTCCAGGCTCCTCATCTATGTTACATCCAGCAGAGGCTGCTGCTCCAGCAGAG 180  
QY 121 CAGGCTCCAGGCTCCTCATCTATGTTACATCCAGCAGAGGCTGCTGCTCCAGCAGAG 180  
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QY 181 TCCAGTGTAGTGGTCTGTCAGCAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTT 240  
Db 241 GATTTTGCAGTGTACTACTGTCAGCAGACTATGTTGGTCTCAGCAGTGG---TTCGCTGAAGG 297  
QY 241 GATTTTGCAGTGTACTACTGTCAGCAGACTATGTTGGTCTCAGCAGTGG---TTCGCTGAAGG 297  
Db 298 ACCAAGTGGAACTCAA 315  
QY 301 ACCAAGTGGAGATCAA 318

RESULT 3  
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AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 2, Application PC/TUS9401258.  
QY Sequence 2, Application PC/TUS9401258  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIPOD LIBRARIES  
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS  
CC NUMBER OF SEQUENCES: 61  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1 0, Version #1 25 (EPO)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US94/01258  
CC FILING DATE: 02-FEB-1994  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/012,566  
CC FILING DATE: 02-FEB-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/174,674







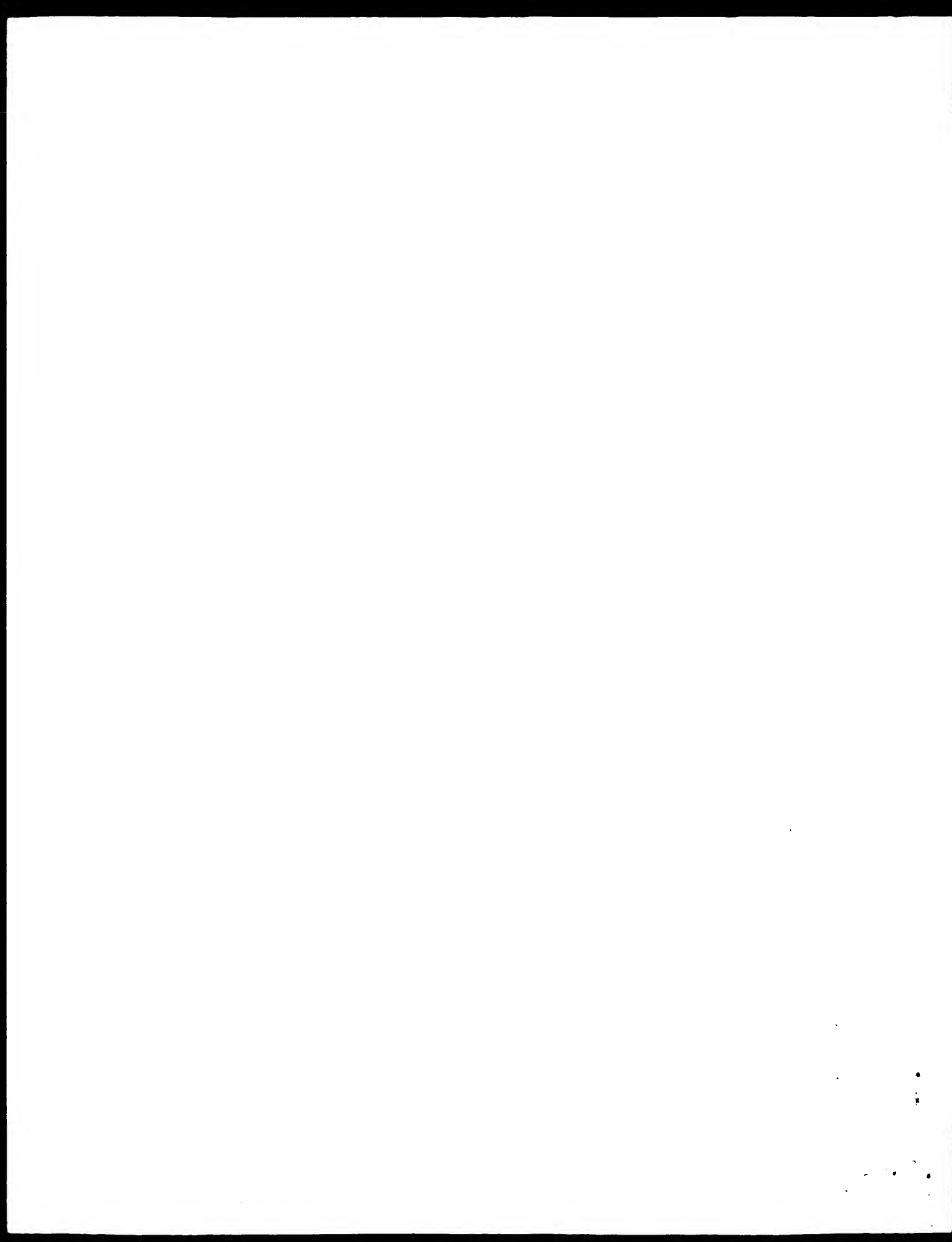












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RESULT 13
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AC P04434;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932.
RA PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL: X02723; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSSP: P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT CHAIN 1 20
FT DOMAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12757 MW; 27FA1BCE CRC32;

Query Match 74.3%; Score 548; DB 5; Length 116;
Best Local Similarity 86.4%; Pred. No. 3.01e-98;
Matches 76; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

Db 24 mtspsltlspsvrlscrasqsvssyltwyqkpkqaprllyqasratrsiparf 83
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 LTOSPATLSLSPGERATLSCRASQSVNK-YLAWYQKPKQAPRLLYDASNPAIGIPARF 61
Db 84 sgsqsgtdftltisslqpedfavyycq 111
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 SGSGSGTDFLTISNLEPEDFAVYVCQ 89

RESULT 14
ID KV1M_HUMAN STANDARD: PRT: 108 AA.
AC P01605;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAV).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 77038198.
RA CAPRA J.D., KLAPPER D.G.;
RL SCAND. J. IMMUNOL. 5:677-684(1976).
CC -!- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01871; K1HULY.
DR HSSP: P01607; 2FCW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 55 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.

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FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 22282B0C CRC32;

Query Match 73.6%; Score 543; DB 5; Length 108;
Best Local Similarity 67.6%; Pred. No. 4.32e-97;
Matches 71; Conservative 21; Mismatches 12; Indels 1; Gaps 1;

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2 ELTQSPATLSLSPGERATLSCRASQSVNKYLAWYQKPKQAPRLLYDASNPAIGIPARF 61
Db 63 sgsqsgtdftltisslqpediatyycqynnwptfgqgtkvevk 107
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 SGSGSGTDFLTISNLEPEDFAVYVCQSRDWV-TFGGKTKVEIK 105

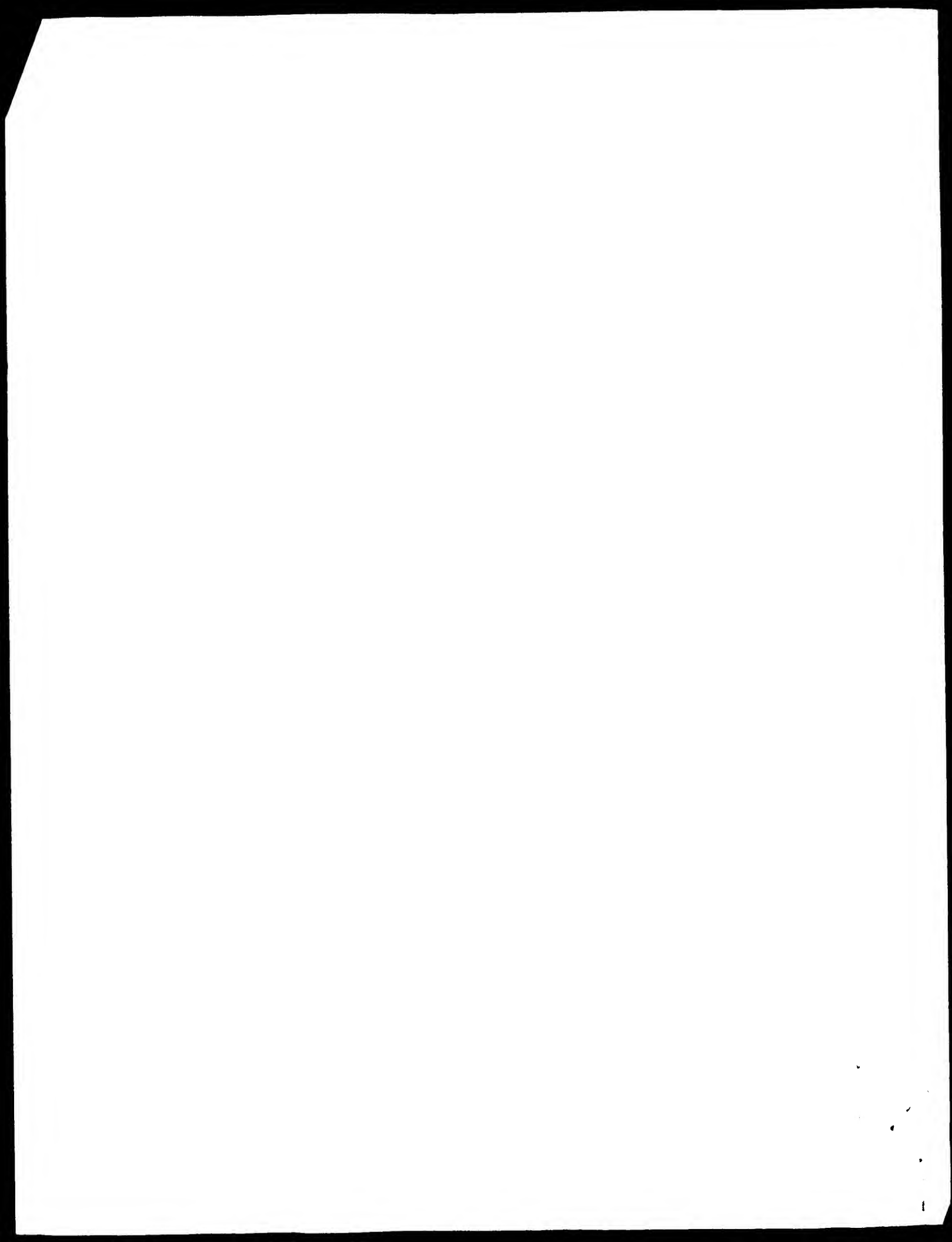
RESULT 15
ID KVID_HUMAN STANDARD: PRT: 107 AA.
AC P01596;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-I REGION (CAR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75075135.
RA MILSTEIN C.P., DEVORSON E.V.;
RL EUR. J. BIOCHEM. 49:377-391(1974).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (1.2) MARKER.
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01864; K1HUAR.
DR HSSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT CARBOHYD 28
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; 04RF9EFD CRC32;

Query Match 71.1%; Score 525; DB 5; Length 107;
Best Local Similarity 63.5%; Pred. No. 6.22e-93;
Matches 66; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Db 3 qmtqpslsvsdvdrvtitocsqsnvaylnwyqkpkglapkllyqasrtreavpsrf 62
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 ELTQSPATLSLSPGERATLSCRASQSVNKYLAWYQKPKQAPRLLYDASNPAIGIPARF 61
Db 63 sgsqsgtdftltisslqpbfbatycqyntfftpgatkvdik 106
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 SGSGSGTDFLTISNLEPEDFAVYVCQSRDWVTFGGKTKVEIK 105

```

Search completed: Tue Feb 24 07:19:20 1998  
Job time : 15 secs.



\*\*\*\*\*  
WIREH (TM)  
\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:19:37 1998: Maspar time 9.55 Seconds

Tabular output not generated. 334,962 Million cell updates/sec

Title: >US-08-844-215-9

Description: (1-105) from US08A44215 pep

Perfect Score: 738

Sequence: 1 AELTQSPATLSLSPGERATL.....VQQQPSDWVTFGGIKVEIK 105

Scoring table: PAM 150

Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir53

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3

8:unann4 9:unann5 10:unann6 11:unann7 12:unann8

13:unann9 14:unann10 15:unann11 16:unann12 17:unann13

18:unrev

Statistics: Mean 40.220; Variance 128.295; scale 0.313

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	695	94.2	108	7	Ig kappa chain V reg	1.85e-71
2	695	93.4	144	7	Ig kappa chain V reg	1.10e-70
3	698	91.9	111	7	Ig kappa chain V reg	2.87e-69
4	675	91.5	128	7	Ig kappa chain V reg	6.99e-69
5	671	90.9	114	7	Ig kappa chain V reg	2.29e-68
6	657	89.0	128	7	Ig kappa light chain	1.44e-66
7	656	88.9	128	7	Ig kappa light chain	1.94e-66
8	655	88.8	125	7	Ig kappa light chain	2.61e-66
9	649	87.9	124	7	Ig kappa light chain	1.54e-65
10	641	86.9	107	7	Ig kappa light chain V reg	1.64e-64
11	631	85.5	108	7	Ig kappa chain V reg	3.14e-63
12	626	84.8	115	7	Ig kappa chain V reg	1.37e-62
13	626	84.8	117	7	Ig kappa chain - hum	1.37e-62
14	620	84.0	115	7	Ig kappa chain precu	8.06e-62
15	617	83.6	108	7	Ig kappa chain V-reg	1.95e-61
16	615	83.3	109	7	Ig kappa chain V-reg	3.52e-61
17	614	83.2	107	7	Ig kappa chain V-reg	4.72e-61
18	612	82.9	129	7	Ig kappa chain - hum	8.52e-61
19	611	82.8	108	7	Ig kappa chain V-reg	1.14e-60
20	611	82.9	129	7	Ig kappa chain V-reg	1.14e-60

21	610	82.7	104	7	PH0964	Ig kappa chain V reg	1.54e-60
22	610	82.7	107	7	S34005	Ig kappa chain V reg	1.54e-60
23	609	82.5	109	7	B30602	Ig kappa chain V-reg	2.06e-60
24	608	82.4	108	7	C30608	Ig kappa chain V-reg	2.77e-60
25	608	82.4	109	7	G30607	Ig kappa chain V-reg	2.77e-60
26	608	82.4	129	7	K3HUG1	Ig kappa chain precu	2.77e-60
27	607	82.2	109	7	F44151	Ig kappa chain V-reg	3.71e-60
28	606	82.1	109	7	C30601	Ig kappa chain V-reg	4.99e-60
29	605	82.0	108	7	B30601	Ig kappa chain V-reg	6.46e-60
30	605	82.0	109	7	K3HUG1	Ig kappa chain V-reg	6.46e-60
31	604	81.8	109	7	F30607	Ig kappa chain V-reg	8.98e-60
32	604	81.8	129	7	K3HUG1	Ig kappa chain precu	8.98e-60
33	603	81.7	110	7	S20635	Ig kappa chain V-reg	1.21e-59
34	602	81.6	109	7	PH0963	Ig kappa chain V-reg	1.62e-59
35	601	81.4	130	7	S40160	Ig kappa chain - hum	2.17e-59
36	600	81.3	109	7	F30601	Ig kappa chain V-reg	2.42e-59
37	600	81.3	109	7	K3HUG1	Ig kappa chain V-reg	2.42e-59
38	599	81.2	109	7	C30601	Ig kappa chain V-reg	3.91e-59
39	599	81.2	109	7	H30601	Ig kappa chain V-reg	3.91e-59
40	596	80.8	109	7	K3HUG1	Ig kappa chain V-reg	5.46e-59
41	595	80.6	109	7	S47181	Ig kappa chain - hum	1.27e-58
42	595	80.6	110	7	F30607	Ig kappa chain V-reg	1.27e-58
43	592	80.2	109	7	K3HUG1	Ig kappa chain V-reg	3.67e-58
44	591	80.1	129	7	S46369	Ig kappa chain V-reg	4.12e-58
45	591	80.1	134	7	S38643	Ig kappa chain V-reg	4.12e-58

ALIGNMENTS

RESULT 1  
ENTRY G44151 #type fragment  
TITLE Ig kappa chain V region (JM-10) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 27-Jun-1994 #sequence\_revision 27-Jun-1994 #ext\_change 15-Aug-1996

ACCESSIONS G44151  
REFERENCE A44151  
#authors Zebeder, S L; Barbas III, C F; Hon, Y I; Caethien, R H; Graff, P J; Dedraw, J J; Pyati, J J; Lapolla, P J; Burton, D P; Lerner, P A; Thornton, G B.  
#journal Proc. Natl. Acad. Sci. U S A (1992) 89:3175-3179  
#title Human combinatorial antibody libraries to hepatitis B surface antigen.  
#accession G44151  
#status preliminary: not compared with conceptual translation  
#molecule\_type mRNA  
#residues 1-108 #label ZEB  
#note nucleotide translation not given  
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin  
SUMMARY #length 108 #checksum 770

Query Match 94.2%; Score 695; DB 7; Length 108;  
Best Local Similarity 93.4%; Pred. No. 1.85e-71;  
Matches 99; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
DB 1 aeltqspatlslspgeratlsrscasqsvslyawyyqkpgqgprillydsanratpaipar 60  
QY 1 AELTQSPATLSLSPGERATLSRCPASQSVNKLAWYDKPKQAPKLLIYUASNPATGIPAR 60  
DB 61 fsgsgsgtdftltisslepedafvyyqqrsmwffsfaggtkveik 106  
QY 61 FSGSGSGTDTTISNLEPEDFAVYVYQQRSDWVTFGGIKVEIK 105

RESULT 2  
ENTRY PL0106 #type fragment  
TITLE Ig kappa chain precursor V-J-C region (IS1) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 30-Jun-1992 #sequence\_revision 30-Jun-1992 #ext\_change 16-Aug-1996  
ACCESSIONS PL0106

```

REFERENCE
#authors Silberstein, L.E.; Litwin, S.; Carmack, C.E.
#journal J. Exp. Med. (1989) 169:1631-1643
#title Relationship of variable region genes expressed by a human B
cell lymphoma secreting pathologic anti-Pr-2 erythrocyte
autoantibodies.
#cross-references MUID:89235583
#accession PLO106
#molecule_type mRNA
#residues 1-144 #label SIL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
21-115 #domain V region #label VRE\
44-54 #region complementarity-determining 1\
70-76 #region complementarity-determining 2\
109-115 #region complementarity-determining 3\
116-127 #domain J region #label JRG\
128-144 #domain C region (fragment) #label CPE
SUMMARY #length 144 #checksum 3523

Query Match 93.4%; Score 689; DB 7; Length 144;
Best Local Similarity 93.3%; Pred. No. 1.10e-70;
Matches 97; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Db 24 ltqspatlsppgeratlsctasqsvsyawyyqgqgqaprllydasnratgiparfs 83
|||||
QY 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQKGQAPRLIYDASNRTATGIPARFS 62
|||||

Db 84 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 127
|||||
QY 63 GSGSGTDFLTISNLEPEDFAVYVCQQRSDW-VTFGGTKVEIK 105
|||||

RESULT 3
ENTRY S23628 #type fragment
TITLE Ig kappa chain V region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
16-Aug-1996
ACCESSIONS S23628
REFERENCE S23623
#authors Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, P.W.; Deftos, M.;
Kozin, F.; Carson, D.A.; Chen, P
#journal J. Exp. Med. (1992) 175:831-842
#title Genetic analysis of self-associating immunoglobulin G
rheumatoid factors from two rheumatoid synovia implicates
an antigen-driven response.
#cross-references MUID:92156804
#accession S23628
#status preliminary
#molecule_type DNA
#residues 1-111 #label OLE
#cross-references EMBL:X59705
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 111 #checksum 3907

Query Match 91.9%; Score 678; DB 7; Length 111;
Best Local Similarity 93.3%; Pred. No. 2.87e-69;
Matches 97; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltqspatlsppgeratlsctasqsvsyawyyqgqgqaprllydasnratgiparfs 63
|||||
QY 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQKGQAPRLIYDASNRTATGIPARFS 62
|||||

Db 64 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 107
|||||
QY 63 GSGSGTDFLTISNLEPEDFAVYVCQQRSDW-VTFGGTKVEIK 105
|||||

RESULT 4
ENTRY S40379 #type complete
TITLE Ig kappa light chain (VJ) - human

```

```

ENTRY A56701 #type fragment
TITLE Ig kappa chain V region precursor (HuA) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
09-May-1997
ACCESSIONS A56701
REFERENCE A56701
#authors Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat,
E.A.
#journal J. Biol. Chem. (1995) 270:12457-12465
#title Human and mouse monoclonal antibodies to blood group A
substance, which are nearly identical immunochemically, use
radically different primary sequences.
#accession A56701
#status preliminary
#molecule_type mRNA
#residues 1-128 #label NIC
#cross-references GB:L41174
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 128 #checksum 6378

Query Match 91.5%; Score 675; DB 7; Length 128;
Best Local Similarity 92.3%; Pred. No. 6.99e-69;
Matches 96; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Db 24 ltqspatlsppgeratlsctasqsvsyawyyqgqgqaprllydasnratgiparfs 83
|||||
QY 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQKGQAPRLIYDASNRTATGIPARFS 62
|||||

Db 84 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 127
|||||
QY 63 GSGSGTDFLTISNLEPEDFAVYVCQQRSDW-VTFGGTKVEIK 105
|||||

RESULT 5
ENTRY S54905 #type fragment
TITLE Ig kappa chain V region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
16-Aug-1996
ACCESSIONS S54905
REFERENCE S54905
#authors Esposito, G.; Traboni, C.
#submission Submitted to the EMBL Data Library, November 1994
#description Cloning and sequencing of cDNA coding for the variable
domains of a human antibody against Hepatitis C virus
helicase.
#accession S54905
#status preliminary
#molecule_type mRNA
#residues 1-114 #label ESP
#cross-references EMBL:X82934
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 114 #checksum 5831

Query Match 90.9%; Score 671; DB 7; Length 114;
Best Local Similarity 91.4%; Pred. No. 2.29e-68;
Matches 96; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 4 mtqspatlsppgeratlsctasqsvsyawyyqgqgqaprllydasnratgiparfs 63
|||||
QY 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQKGQAPRLIYDASNRTATGIPARFS 62
|||||

Db 64 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 108
|||||
QY 63 GSGSGTDFLTISNLEPEDFAVYVCQQRSDW-VTFGGTKVEIK 105
|||||

RESULT 6
ENTRY S40379 #type complete
TITLE Ig kappa light chain (VJ) - human

```





Paterson, G.; Willison, G.; Kennedy, P.G.E.; Willison, H.J.  
 submitted to the EMBL Data Library, June 1995  
 Analysis of anti-GM1 ganglioside IgM antibodies cloned from  
 motor neuropathy patients demonstrates diverse variable  
 region gene usage with extensive somatic mutation.

#accession S57444  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-107 #label PAT  
 #cross-references EMBL:X87898  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 107 #checksum 7400

Query Match 86.9%; Score 641; DB 7; Length 107;  
 Best Local Similarity 87.5%; Pred. No. 1.64e-64;  
 Matches 91; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 4 ltgspatlslsperatlscrasqsvstylaayqkpgqgslliydasnraagaiaarfs 63  
 QY 3 LTQSPATLSLSPGERATLSCRASQSVNKYLAAYQKPGQAPRLIYDASNRATGIPARFS 62  
 Db 64 gsgsgtdftltisslepedfavyvccqrsnwpptfgggtvvesk 107  
 QY 63 GSGSGTDFTLTISNLEPEDFAVYVCQQRSDWV-TFGGTRKVEIK 105

RESULT 11  
 ENTRY H44151 #type fragment  
 TITLE Ig kappa chain V region (JM-15) - human (fragment)  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 16-Aug-1996

ACCESSIONS H44151  
 REFERENCE A44151  
 #authors Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.;  
 Graff, R.; DeGraw, J.; Pyatt, J.; Lapolla, R.; Burton,  
 D.R.; Lerner, R.A.; Thornton, G.B.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179  
 #title Human combinatorial antibody libraries to hepatitis B surface  
 antigen.

#accession H44151  
 #status preliminary; not compared with conceptual translation  
 #molecule\_type mRNA  
 #residues 1-108 #label ZEB  
 #note nucleotide translation not given  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS heterotetramer; immunoglobulin  
 SUMMARY #length 108 #checksum 1576

Query Match 85.5%; Score 631; DB 7; Length 108;  
 Best Local Similarity 86.8%; Pred. No. 3.14e-63;  
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 aeltspatlslsperatlscrasqsvssylaayqkpgqaprlliygastatgipd 60  
 QY 1 AELTSPATLSLSPGERATLSCRASQSVNK-YLAAYQKPGQAPRLIYDASNRATGIPA 59

Db 61 rfsgsgtdftltisslepedfavyvccqgsptfgggtkvelk 106  
 QY 60 RFGSGTDFTLTISNLEPEDFAVYVCQQRSDWVTFGGTRKVEIK 105

RESULT 12  
 ENTRY K3HUVG #type complete  
 TITLE Ig kappa chain precursor V-III region (Vg) - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 06-Sep-1996

ACCESSIONS A01900  
 REFERENCE A93549  
 #authors Pech, M.; Zachau, H.G.  
 #journal Nucleic Acids Res. (1984) 12:9229-9236  
 #title Immunoglobulin genes of different subgroups are

interdigitated within the V-K locus.  
 #cross-references MUID:85087932  
 #accession A01900  
 #molecule\_type DNA  
 #residues 1-115 #label PEC  
 #note the sequence was determined from the germline gene

GENETICS  
 #gene GDB:IGKV3  
 #cross-references GDB:136266  
 #introns 17/1  
 #intron 17/1  
 #complex An immunoglobulin heterotetramer subunit consists of two  
 identical light (kappa or lambda) and two identical heavy  
 (alpha, delta, epsilon, gamma, or mu) chains usually  
 stabilized by interchain disulfide bonds. In some cases,  
 such as IgA and IgM, the subunits associate into larger  
 oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS heterotetramer; immunoglobulin  
 FEATURE  
 1-20 #domain signal sequence #status predicted #label SIG\  
 21-115 #product Ig kappa chain V-III region (Vg) #status  
 Predicted #label MAT\  
 21-43 #region framework 1\  
 44-54 #region complementarity-determining 1\  
 55-69 #region framework 2\  
 70-76 #region complementarity-determining 2\  
 77-108 #region framework 3\  
 109-115 #region complementarity-determining 3\  
 43-108 #disulfide\_bonds #status predicted  
 SUMMARY #length 115 #molecular\_weight 12575 #checksum 8230

Query Match 84.8%; Score 626; DB 2; Length 115;  
 Best Local Similarity 95.6%; Pred. No. 1.37e-62;  
 Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltgspatlslsperatlscrasqsvssylaayqkpgqaprlliydasnratgiparfs 83  
 QY 3 LTQSPATLSLSPGERATLSCRASQSVNKYLAAYQKPGQAPRLIYDASNRATGIPARFS 62

Db 84 gsgsgtdftltisslepedfavyvccqrsn 114  
 QY 63 GSGSGTDFTLTISNLEPEDFAVYVCQQRSDW 93

RESULT 13  
 ENTRY S40362 #type complete  
 TITLE Ig kappa chain - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 16-Aug-1996

ACCESSIONS S40362  
 REFERENCE S40312  
 #authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
 #journal Eur. J. Immunol. (1993) 23:3248-3271  
 #title Expressed human immunoglobulin chi genes and their  
 hypermutation.

#accession S40362  
 #status preliminary; translation not shown  
 #molecule\_type mRNA  
 #residues 1-117 #label KLE  
 #cross-references EMBL:X72472  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin  
 KEYWORDS heterotetramer; immunoglobulin  
 SUMMARY #length 117 #molecular\_weight 12613 #checksum 8309

Query Match 84.8%; Score 626; DB 7; Length 117;  
 Best Local Similarity 84.6%; Pred. No. 1.37e-62;  
 Matches 88; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 14 mtgspatlslsperatlscrasqsvssnlaayqkpgqaprlliygastatgiparfs 73  
 QY 3 LTQSPATLSLSPGERATLSCRASQSVNKYLAAYQKPGQAPRLIYDASNRATGIPARFS 62

Db 74 usgsqtdftltlisslepedfavyvqqgynwpltfqgatkveik 117  
 QY 63 GSGSGTDTLTLSNLEPEDFAVYVQQQSDW-VIFGSGTKVEIK 105

## RESULT 14

ENTRY S11697 #type complete  
 TITLE Ig kappa chain precursor V-III region - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
 ACCESSIONS S11697  
 REFERENCE S11697  
 #authors Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.  
 #journal J. Mol. Biol. (1995) 183:291-299  
 #title A large section of the gene locus encoding human immunoglobulin variable regions of the kappa type is duplicated.  
 #cross-references MUID:85264787  
 #accession S11697  
 #status preliminary; nucleic acid sequence not shown; translation not shown  
 ##molecule\_type DNA  
 ##residues 1-115 ##label PEC  
 ##cross-references EMBL:X17264  
 ##note the nucleotide sequence was submitted to the EMBL Data Library, December 1989

## GENETICS

#introns 17/1  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS heterotetramer; immunoglobulin  
 SUMMARY #length 115 #molecular\_weight 12599 #checksum 7620

Query Match 84.0%; Score 620; DB 7; Length 115;  
 Best Local Similarity 93.4%; Pred. No. 8.06e-62;  
 Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsqgeratlsqrasqvsnylawyqkqgqaprllydcastratgiparfs 83  
 QY 3 LTQSPATLSLSPGERATLSQFASQSVN-KYLAWYQKQGAPRLLYDASNPATGIPAPFS 62

Db 84 qsgqgtdftltlisslepedfavyvqqrsnw 114  
 QY 63 GSGSGTDTLTLSNLEPEDFAVYVQQQSDW 93

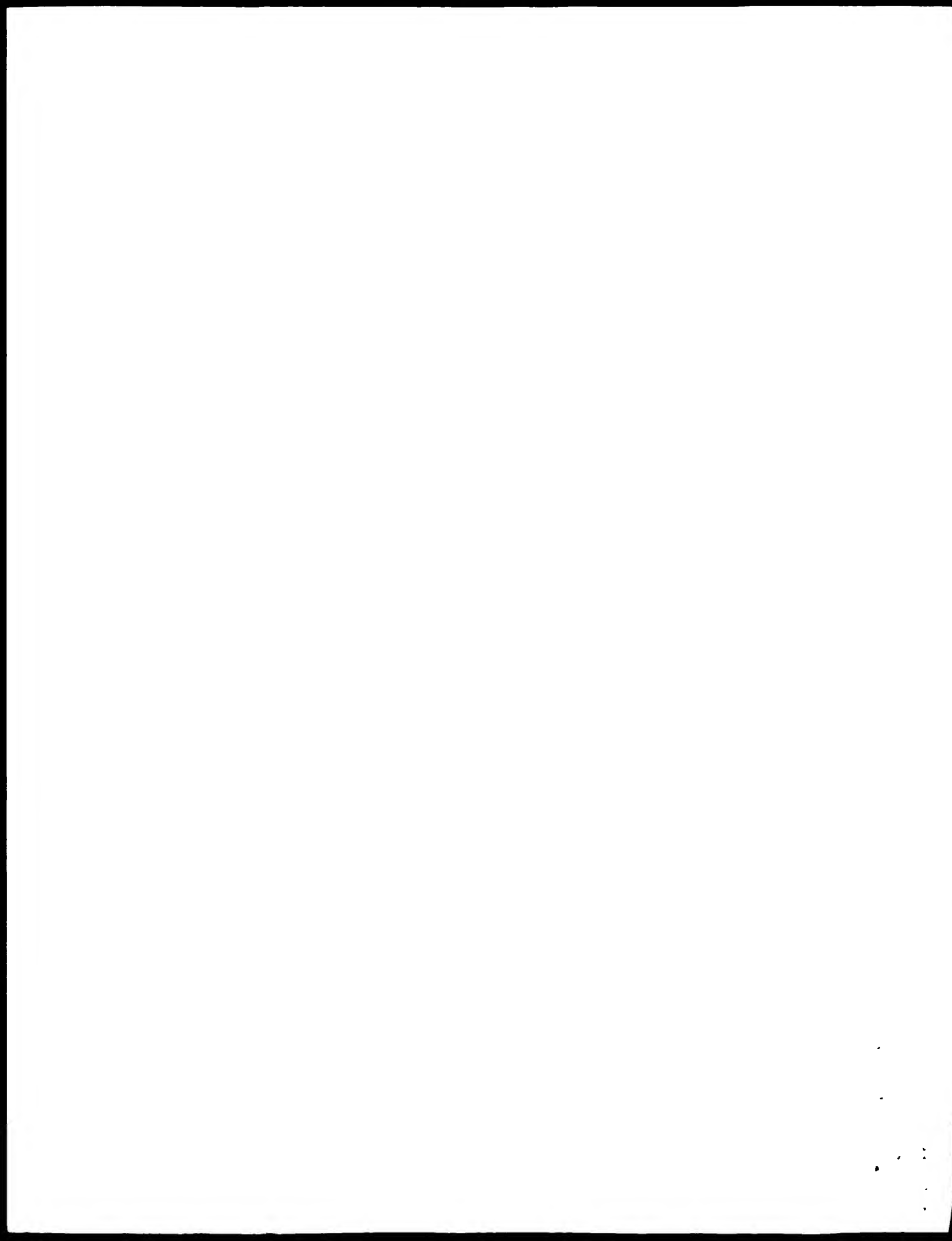
## RESULT 15

ENTRY E30609 #type fragment  
 TITLE Ig kappa chain V-III region (Jh) - human (fragment)  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
 ACCESSIONS E30609  
 REFERENCE A30601  
 #authors Goni, F. P.; Chen, P. P.; McGinnis, D.; Arjonilla, M. L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, R.  
 #journal J. Immunol. (1989) 142:3158-3163  
 #title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.  
 #cross-references MUID:89215279  
 #accession E30609  
 #status preliminary  
 ##molecule\_type protein  
 ##residues 1-108 ##label GON  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS heterotetramer; immunoglobulin  
 SUMMARY #length 108 #checksum 199

Query Match 83.6%; Score 617; DB 7; Length 108;  
 Best Local Similarity 84.6%; Pred. No. 1.95e-61;  
 Matches 88; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Db 4 ltqspatlsqgeratlsqrasqvsnylawyqkqgqaprllydcastratgiparfs 83  
 QY 3 LTQSPATLSLSPGERATLSQFASQSVN-KYLAWYQKQGAPRLLYDASNPATGIPAPFS 62  
 Db 64 sgsqsgtdftltlisslepedfavyvqqgfnspsfqgatkveik 107  
 QY 62 SSGSGTDTLTLSNLEPEDFAVYVQQQSDW-VIFGSGTKVEIK 105

Search completed: Tue Feb 24 07:19:49 1998  
 Job time : 12 secs.



\*\*\*\*\*  
WIRE (TM)  
\*\*\*\*\*

Release 2.12 John F. Collins, BioComputing Research Unit  
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.  
Distribution rights by IntelliGenetics, Inc.  
MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:46:01 1998. Maspar time 3.01 Seconds  
Tabular output not generated.  
Title: >US-08-844-215-9  
Description: (1-105) from US08844215.pep  
Perfect Score: 738  
Sequence: 1 AELTQSPATLSLSPGERATL.....YQQRSDWVTFGGIKVEIK 105

Scoring table: PAM 150  
Gap 11  
Searched: 56402 seqs, 5095871 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59  
10:PCR92 11:PCR93 12:PCR94 13:PCR95 14:PCR96  
Statistics: Mean 27.520, Variance 149.406, scale 0.184  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	626	84	8	115	US-08-053- Sequence 179, Applicat	4	48e-39
2	620	84	0	115	US-08-053- Sequence 181, Applicat	1	30e-38
3	615	83	5	109	US-08-053- Sequence 147, Applicat	2	65e-38
4	615	83	5	109	US-08-276- Sequence 147, Applicat	2	65e-38
5	608	82	4	111	US-08-276- Sequence 149, Applicat	1	10e-37
6	609	82	4	111	US-08-276- Sequence 149, Applicat	1	10e-37
7	605	82	1	107	US-08-276- Sequence 90, Applicat	1	56e-37
8	605	82	1	107	US-08-276- Sequence 90, Applicat	1	56e-37
9	605	82	0	108	US-08-276- Sequence 86, Applicat	1	87e-37
10	605	82	0	108	US-08-276- Sequence 86, Applicat	1	87e-37
11	600	81	3	108	US-08-477- Sequence 86, Applicat	4	54e-37
12	600	81	3	108	US-08-477- Sequence 86, Applicat	4	54e-37
13	600	81	3	108	US-08-474- Sequence 86, Applicat	4	54e-37
14	600	81	3	108	US-08-474- Sequence 86, Applicat	4	54e-37
15	594	80	5	107	US-08-276- Sequence 87, Applicat	1	32e-36
16	594	80	5	107	US-08-276- Sequence 87, Applicat	1	32e-36
17	594	80	5	108	US-08-276- Sequence 86, Applicat	1	32e-36
18	594	80	5	108	US-08-276- Sequence 86, Applicat	1	32e-36
19	593	80	4	104	US-08-276- Sequence 99, Applicat	1	57e-36
20	593	80	4	104	US-08-276- Sequence 99, Applicat	1	57e-36
21	591	80	1	105	US-08-276- Sequence 100, Applicat	1	57e-36
22	585	79	3	108	US-08-276- Sequence 110, Applicat	6	44e-36

23	585	79	3	108	13	PCT-US95-0	Sequence 110, Applicat	6	44e-36
24	583	79	0	103	11	PCT-US95-0	Sequence 24, Applicat	9	26e-36
25	581	78	7	107	6	US-07-634-	Sequence 63, Applicat	1	32e-35
26	581	78	7	107	6	US-07-634-	Sequence 63, Applicat	1	32e-35
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28	581	78	7	107	7	US-08-474-	Sequence 67, Applicat	1	32e-35
29	581	78	7	107	6	US-08-477-	Sequence 67, Applicat	1	32e-35
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31	581	78	7	107	7	US-08-477-	Sequence 67, Applicat	1	32e-35
32	581	78	7	107	7	US-08-477-	Sequence 67, Applicat	1	32e-35
33	566	76	7	104	13	PCT-US95-0	Sequence 94, Applicat	1	88e-34
34	566	76	7	104	7	US-08-276-	Sequence 94, Applicat	1	88e-34
35	564	76	4	108	7	US-08-276-	Sequence 96, Applicat	1	88e-34
36	564	76	4	108	13	PCT-US95-0	Sequence 96, Applicat	2	68e-34
37	563	76	3	112	13	PCT-US95-0	Sequence 151, Applicat	3	20e-34
38	563	76	3	112	7	US-08-276-	Sequence 151, Applicat	3	20e-34
39	562	76	2	116	7	US-09-053-	Sequence 183, Applicat	8	76e-34
40	558	75	6	108	7	US-08-276-	Sequence 88, Applicat	7	76e-34
41	558	75	6	108	13	PCT-US95-0	Sequence 88, Applicat	7	76e-34
42	546	74	0	107	11	PCT-US95-0	Sequence 18, Applicat	6	48e-33
43	543	73	6	107	6	US-07-634-	Sequence 34, Applicat	1	10e-32
44	543	73	6	107	6	US-08-477-	Sequence 34, Applicat	1	10e-32
45	543	73	6	107	7	US-08-477-	Sequence 34, Applicat	1	10e-32

ALIGNMENTS

RESULT 1  
ID US-08-053-131-179 STANDARD: PRT: 115 AA.  
XX  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 179, Application US/08053131.  
XX  
CC Sequence 179, Application US/08053131  
CC Patent No. 5661016  
CC GENERAL INFORMATION:  
CC APPLICANT: Lonberg, Nils  
CC APPLICANT: Kay, Robert M.  
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
CC TITLE OF INVENTION: Producing Heterologous Antibodies  
CC NUMBER OF SEQUENCES: 197  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Townsend and Townsend Koorie and Crew  
CC STREET: One Market Plaza, Stewart Tower, Suite 200  
CC CITY: San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94105  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/053,131  
CC FILING DATE: 26-APR-1993  
CC CLASSIFICATION: 800  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/990,860  
CC FILING DATE: 16-DEC-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/810,279  
CC FILING DATE: 17-DEC-1991  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/953,408  
CC FILING DATE: 18-MAR-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/WORK NUMBER: 14443-9-3

CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-326-2400  
CC TELEFAX: 415-326-2422

CC INFORMATION FOR SEQ ID NO: 179:  
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 115 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear

CC MOLECULE TYPE: protein  
CC SEQUENCE 115 AA; 12575 MW; 71214 CN;

Query Match 84.8%; Score 626; DB 7; Length 115;  
Best Local Similarity 95.6%; Pred. No. 4.48e-39;  
Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 83  
|||||  
Qy 3 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 62  
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Db 84 GSGGTDFTLTISLLEPEDFAVYQCQRSDW 114  
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Qy 63 GSGGTDFTLTISLLEPEDFAVYQCQRSDW 93  
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RESULT 2

ID US-08-053-131-181 STANDARD: PRT: 115 AA.

XX AC

XX xxxxxx

DT 01-JAN-1900

DE Sequence 181, Application US/08053131.

XX

CC Sequence 181, Application US/08053131

CC Patent No. 5661016

CC GENERAL INFORMATION:

CC APPLICANT: Lonberg, Nils

CC APPLICANT: Kay, Robert M.

CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for

CC TITLE OF INVENTION: Producing Heterologous Antibodies

CC NUMBER OF SEQUENCES: 197

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend Khoultie and Crew

CC STREET: One Market Plaza, Steuart Tower, Suite 200

CC CITY: San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94105

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/053,131

CC FILING DATE: 26-APR-1993

CC CLASSIFICATION: 800

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/990,860

CC FILING DATE: 16-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/910,279

CC FILING DATE: 17-DEC-1991

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/853,408

CC FILING DATE: 18-MAR-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Smith, William M.

CC REGISTRATION NUMBER: 30,223

CC REFERENCE/DOCKET NUMBER: 14643-Q-3

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415-326-2400

CC TELEFAX: 415-326-2422

CC INFORMATION FOR SEQ ID NO: 181:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 115 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 115 AA; 12599 MW; 70085 CN;

Query Match 84.0%; Score 620; DB 7; Length 115;

Best Local Similarity 93.4%; Pred. No. 1.30e-38;

Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 83  
|||||

Qy 3 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 62  
|||||

Db 84 GSGGTDFTLTISLLEPEDFAVYQCQRSDW 114  
|||||

Qy 63 GSGGTDFTLTISLLEPEDFAVYQCQRSDW 93  
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RESULT 3

ID PCT-US95-08743-147 STANDARD: PRT: 109 AA.

XX AC

XX xxxxxx

DT 01-JAN-1900

DE Sequence 147, Application PC/TUS9508743.

CC Sequence 147, Application PC/TUS9508743

CC GENERAL INFORMATION:

CC APPLICANT:

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/08743

CC FILING DATE: 11-JUL-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/276,852

CC FILING DATE: 18-JUL-1994

CC INFORMATION FOR SEQ ID NO: 147:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 109 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 109 AA; 11779 MW; 65550 CN;

Query Match 83.5%; Score 616; DB 13; Length 109;

Best Local Similarity 84.9%; Pred. No. 2.65e-38;

Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Db 2 AELTSPGILSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPD 61  
|||||

Qy 1 AELTSPGILSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPD 59  
|||||

Db 62 RFGSGGTDFTLTISLLEPEDFAVYQCQRSDW 107  
|||||

Qy 60 RFGSGGTDFTLTISLLEPEDFAVYQCQRSDW 105  
|||||

RESULT 4

ID US-08-276-852-147 STANDARD: PRT: 109 AA.

XX AC

XX xxxxxx

XX

DT 01-JAN-1900  
 XX Sequence 147, Application US/08276852.  
 DE Patent No. 5652138  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Burton, Dennis R  
 CC APPLICANT: Barbas, Carlos F  
 CC APPLICANT: Lerner, Richard A  
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Scripps Research Institute, Office of  
 CC ADDRESSEE: Patent Counsel  
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent In Release #1 0, Version #1 25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCRI452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 147:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 109 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 109 AA; 11779 MW; 65550 CN;  
 Query Match 83.5%; Score 616; DB 7; Length 109;  
 Best Local Similarity 84.9%; Pred No 2 65e-3a  
 Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;  
 Db 2 AELTSPGTLSPGERVIVSCRASQSVSNLYAWYQKFGQAPRLIYGASNRATGIPD 61  
 QY 1 AELTSPATLSLSPGERATLSCRASQSVSN-KYLAWYQKFGQAPRLIYGASNRATGIPA 59  
 Db 62 RFGSGSGTDFTLTISLRLPEDEFAVYVCOQYSGSGTGGTKVEIK 107  
 QY 60 RFGSGSGTDFTLTISLRLPEDEFAVYVCOQASDWVTFGGTKVEIK 105  
 RESULT 5  
 ID US-08-276-852-149 STANDARD: PRT: 111 AA.  
 XX xxxxxx  
 AC  
 XX 01-JAN-1900  
 DT Sequence 149, Application US/08276852.  
 DE

XX Sequence 149, Application US/08276852  
 CC Patent No. 5652138  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Burton, Dennis R  
 CC APPLICANT: Barbas, Carlos F  
 CC APPLICANT: Lerner, Richard A  
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Scripps Research Institute, Office of  
 CC ADDRESSEE: Patent Counsel  
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCRI452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 149:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 111 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 111 AA; 11956 MW; 63169 CN;  
 Query Match 82.4%; Score 608; DB 7; Length 111;  
 Best Local Similarity 83.0%; Pred. No. 1.10e-37;  
 Matches 88; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
 Db 2 AELTSPGTLSPGERATLSCRASQSVSNLYAWYQKFGQAPRLIYGASNRATGIPD 61  
 QY 1 AELTSPATLSLSPGERATLSCRASQSVSN-KYLAWYQKFGQAPRLIYGASNRATGIPA 59  
 Db 62 RFGSGSGDAFTLTISLRLPEDEFAVYVCOQYSGSGTGGTKVEIK 107  
 QY 60 RFGSGSGTDFTLTISLRLPEDEFAVYVCOQPSWVTFGGTKVEIK 105  
 RESULT 6  
 ID PCT-US95-08743-149 STANDARD: PRT: 111 AA.  
 XX xxxxxx  
 AC  
 XX 01-JAN-1900  
 DT Sequence 149, Application PC/TUS9508743.  
 DE Sequence 149, Application PC/TUS9508743  
 CC GENERAL INFORMATION:

CC APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US95/08743  
 CC FILING DATE: 11-JUL-1995  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC INFORMATION FOR SEQ ID NO: 149:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 111 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 111 AA: 11956 MW; 63169 CN;  
 CC  
 CC Query Match 82.1%; Score 606; DB 13; Length 107;  
 CC Best Local Similarity 83.0%; Pred. No. 1.10e-37;  
 CC Matches 88; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
 CC  
 DB 2 AELTQSPGTLSPGPRATISCRASQSVNSYLAWYQKPGQAPRLIYCASTPATDIPD 61  
 QY 1 AELTQSPATLSLSPGPRATISCRASQSVNK-YLAWYQKPGQAPRLIYDASNRATGIPAR 59  
 DB 62 FSGGSGGDTFTLTISNLEPDEFVAVYCCQQRSDMWVTFGGGKVEIK 107  
 QY 60 FSGGSGGDTFTLTISNLEPDEFVAVYCCQQRSDMWVTFGGGKVEIK 105  
 CC  
 RESULT 7  
 ID PCT-US95-08743-90 STANDARD; PRT; 107 AA.  
 CC  
 CC XXXXXX  
 CC  
 CC 01-JAN-1900  
 CC  
 CC Sequence 90, Application PC/TUS9508743.  
 CC  
 CC Sequence 90, Application PC/TUS9508743  
 CC  
 CC GENERAL INFORMATION:  
 CC APPLICANT:  
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC NUMBER OF SEQUENCES: 170  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US95/08743  
 CC FILING DATE: 11-JUL-1995  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC INFORMATION FOR SEQ ID NO: 90:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 107 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 107 AA: 11705 MW; 62938 CN;  
 CC  
 CC Query Match 82.1%; Score 606; DB 13; Length 107;  
 CC Best Local Similarity 82.1%; Pred. No. 1.56e-37;  
 CC Matches 87; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

DB 1 ELTQSPGTLSPGPRATISCRASQSVNSYLAWYQKPGQAPRLIYGSSTPATDIPD 60  
 QY 2 ELTQSPATLSLSPGPRATISCRASQSV-NKYLAWYQKPGQAPRLIYDASNRATGIPAR 60  
 DB 61 FSGGSGGDTFTLTISNLEPDEFVAVYCCQHYGNSVYTFGGGKLEIK 106  
 QY 61 FSGGSGGDTFTLTISNLEPDEFVAVYCCQPSNWV-TFGGSKVEIK 105  
 CC  
 RESULT 8  
 ID US-08-276-852-90 STANDARD; PRT; 107 AA.  
 CC  
 CC XXXXXX  
 CC  
 CC 01-JAN-1900  
 CC  
 CC Sequence 90, Application US/08276852.  
 CC  
 CC Sequence 90, Application US/08276852  
 CC Patent No. 5652138  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Burton, Dennis R  
 CC APPLICANT: Barbas, Carlos F  
 CC APPLICANT: Lerner, Richard A  
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Scripps Research Institute, Office of  
 CC STREET: 10556 No. 5852138th Torrey Pines Road, Suite 220,  
 CC STREET: Mail Drop IPC8  
 CC CITY: La Jolla  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 92037  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCP1452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 90:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 107 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 107 AA: 11705 MW; 62938 CN;  
 CC  
 CC Query Match 82.1%; Score 606; DB 7; Length 107;  
 CC Best Local Similarity 82.1%; Pred. No. 1.56e-37;  
 CC Matches 87; Conservative 10; Mismatches 7; Indels 2; Gaps 2;





CC COUNTRY: US  
CC ZIP: 94111  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/477,728  
CC FILING DATE: 07-JUN-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/634,278  
CC FILING DATE: 19-DEC-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/590,274  
CC FILING DATE: 28-SEP-1990  
CC APPLICATION NUMBER: US 07/310,252  
CC FILING DATE: 13-FEB-1989  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/290,975  
CC FILING DATE: 28-DEC-1988  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-002600  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 326-2422  
CC INFORMATION FOR SEQ ID NO: 86:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;  
SQ  
Query Match 81.3%; Score 600; DB 6; Length 108;  
Best Local Similarity 84.8%; Pred. No. 4.54e-37;  
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;  
Db 4 LTQSPGTLSPGERATLSRPSQSVSSGVLGWYQKPGQAPPLIYGASSRATGIPDPF 63  
QY 3 LTQSPATLSLSPGERATLSRPSQSVNK-YLAWYQKPGQAPPLIYDASNATGIPAPF 61  
Db 64 SGSGSGTDTLTISRLEPEDFAVYCYQYQSLGRTEFGQGTKEIK 108  
QY 62 SGSGSGTDTLTISNLEPEDFAVYCYQQRSDWV-TEGGGTKEIK 105  
RESULT 12  
ID US-07-634-278-86 STANDARD; PRT: 108 AA.  
XX xxxxxx  
AC  
XX  
XX  
DT 01-JAN-1900  
DE Sequence 86, Application US/07634278.  
XX  
CC Sequence 86, Application US/07634278  
CC Patent No. 5530101  
CC GENERAL INFORMATION:  
CC APPLICANT: QUEEN, Cary L.  
CC APPLICANT: CO. Man Sung  
CC APPLICANT: SCHNEIDER, William P.  
CC APPLICANT: LANDOLFI, Nicholas F.  
CC APPLICANT: COELING, Kathleen L.  
CC APPLICANT: SELICK, Harold E.  
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
CC NUMBER OF SEQUENCES: 113  
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend Kourie and Crew  
CC STREET: 379 Lytton Avenue  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: US  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/634,278  
CC FILING DATE: 19-DEC-1990  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/590,274  
CC FILING DATE: 28-SEP-1990  
CC APPLICATION NUMBER: US 07/310,252  
CC FILING DATE: 13-FEB-1989  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/290,975  
CC FILING DATE: 28-DEC-1988  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-002600  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 326-2422  
CC INFORMATION FOR SEQ ID NO: 86:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;  
SQ  
Query Match 81.3%; Score 600; DB 6; Length 108;  
Best Local Similarity 84.8%; Pred. No. 4.54e-37;  
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;  
Db 4 LTQSPGTLSPGERATLSRPSQSVSSGVLGWYQKPGQAPPLIYGASSRATGIPDPF 63  
QY 3 LTQSPATLSLSPGERATLSRPSQSVNK-YLAWYQKPGQAPPLIYDASNATGIPAPF 61  
Db 64 SGSGSGTDTLTISRLEPEDFAVYCYQYQSLGRTEFGQGTKEIK 108  
QY 62 SGSGSGTDTLTISNLEPEDFAVYCYQQRSDWV-TEGGGTKEIK 105  
RESULT 13  
ID US-08-474-040-86 STANDARD; PRT: 108 AA.  
XX xxxxxx  
AC  
XX  
XX  
DT 01-JAN-1900  
DE Sequence 86, Application US/08474040.  
XX  
CC Sequence 86, Application US/08474040  
CC Patent No. 5693761  
CC GENERAL INFORMATION:  
CC APPLICANT: QUEEN, Cary L.  
CC APPLICANT: CO. Man Sung  
CC APPLICANT: SCHNEIDER, William P.  
CC APPLICANT: LANDOLFI, Nicholas F.  
CC APPLICANT: COELING, Kathleen L.  
CC APPLICANT: SELICK, Harold E.  
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
CC NUMBER OF SEQUENCES: 113  
CC CORRESPONDENCE ADDRESS:

CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Townsend and Townsend Khourie and Crew  
CC STREET: 379 Lytton Avenue  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: US  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/474,040  
CC FILING DATE: 07-JUN-1995  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/634,278  
CC FILING DATE: 19-DEC-1990  
CC APPLICATION NUMBER: US 07/590,274  
CC FILING DATE: 28-SEP-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/310,252  
CC FILING DATE: 13-FEB-1989  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/290,975  
CC FILING DATE: 28-DEC-1988  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-002600  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 326-2422  
CC INFORMATION FOR SEQ ID NO: 86:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 81.3%; Score 600; DB 7; Length 108;  
Best Local Similarity 84.8%; Pred. No. 4.54e-37;  
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 LTQSPGTLSPGEPATLSCPASQSVSSGYLQWYQKPGQAPPLLIYGASSPATGIPDPF 63  
QY 3 LTQSPATLSPGEPATLSCPASQSVNK-YLAWYQKPGQAPPLLIYDASNRATGIPARF 61  
Db 64 SSGSGTDTLTISLPEDEFAVYQCYGSLGTFQGGTKVEIK 108  
QY 62 SSGSGTDTLTISLPEDEFAVYQCYGSLGTFQGGTKVEIK 105

RESULT 14  
ID US-08-487-200-86 STANDARD: PRT: 108 AA  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900

DE Sequence 86, Application US/08487200.  
CC Sequence 86, Application US/08487200  
CC Patent No. 5693762  
CC GENERAL INFORMATION:  
CC APPLICANT: QUEEN, Cary L.  
CC APPLICANT: CO, Man Sung  
CC APPLICANT: SCHNEIDER, William P.  
CC APPLICANT: LANDOLF, Nicholas F.  
CC APPLICANT: BELINGH, Kathleen L.

CC APPLICANT: SELICK, Harold E.  
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
CC NUMBER OF SEQUENCES: 113  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Townsend and Townsend and Crew  
CC STREET: 379 Lytton Avenue  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: US  
CC ZIP: 94301

CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/487,200  
CC FILING DATE: 7-JUN-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/634,278  
CC FILING DATE: 19-DEC-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/590,274  
CC FILING DATE: 28-SEP-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/310,252  
CC FILING DATE: 13-FEB-1989  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/290,975  
CC FILING DATE: 28-DEC-1988  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M.  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-002610  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 326-2422  
CC INFORMATION FOR SEQ ID NO: 86:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 81.3%; Score 600; DB 7; Length 108;  
Best Local Similarity 84.8%; Pred. No. 4.54e-37;  
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 LTQSPGTLSPGEPATLSCPASQSVSSGYLQWYQKPGQAPPLLIYGASSPATGIPDPF 63  
QY 3 LTQSPATLSPGEPATLSCPASQSVNK-YLAWYQKPGQAPPLLIYDASNRATGIPARF 61  
Db 64 SSGSGTDTLTISLPEDEFAVYQCYGSLGTFQGGTKVEIK 108  
QY 62 SSGSGTDTLTISLPEDEFAVYQCYGSLGTFQGGTKVEIK 105

RESULT 15  
ID PCT-US95-08743-87 STANDARD: PRT: 107 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900

DE Sequence 87, Application PCT/TUS9508743.  
CC Sequence 87, Application PCT/TUS9508743  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 CC NUMBER OF SEQUENCES: 170  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent in Release #1.0, Version #1 25 (EPO)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US95/08743  
 CC FILING DATE: 11-JUL-1995  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC INFORMATION FOR SEQ ID NO: 87:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 107 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 107 AA; 11654 MW; 62438 CN;

Query Match 80.5%; Score 594; DB 13; Length 107;  
 Best Local Similarity 83.0%; Pred. No. 1.32e-36;  
 Matches 88; Conservative 8; Mismatches 8; Indels 2; Gaps 2;  
 Db 1 ELTQSPGTLSPGPRATLSGRASQSVSNVYLAWYQOPGQAPPLLIYGASNEATGIPDR 60  
 QY 2 ELTQSPATLSLSPGPRATLSGRASQSV-NKYLAWYQOPGQAPPLLIYDASNPATGIPAR 60  
 Db 61 FSGSGGTAFITLTISSLOPEDVAIYQQVHSSPYTFGGTKLEIK 106  
 QY 61 FSGSGGTDFLTITISNLEPEDFAVYVCOQ-RSDWVTEGGTKVEIK 105

Search completed: Tue Feb 24 07:46:22 1998  
 Job time : 21 secs.

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W P E R E H

(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:20:07 1998; MasPar time 5.74 Seconds  
Tabular output not generated. 215.418 Million cell updates/sec

Title: >US-08-844-215-9  
Description: (1-105) from US08844215.ppt  
Perfect Score: 738  
Sequence: 1 AELIUSPAILSLSPERAIL.....YCCGRSDWVIFGGTKVEIK 105

Scoring table: PAM 150  
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq30  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 30.157; Variance 177.084; scale 0.170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	Query Match	Length	ID	Description	Pred. No.
1	549	87.9	349	2	R12128	1.11e-36
2	549	87.9	401	2	R12128	1.11e-36
3	549	87.9	414	2	R12128	1.11e-36
4	549	87.9	414	2	R12128	1.11e-36
5	525	84.8	115	7	R38648	4.82e-35
6	526	84.8	115	11	R62928	4.82e-35
7	526	84.8	120	20	W03945	4.82e-35
8	520	84.0	115	7	R38648	4.82e-35
9	520	84.0	115	11	R62928	4.82e-35
10	520	84.0	115	20	W03945	4.82e-35
11	615	83.5	109	10	W03947	1.29e-34
12	616	83.5	109	19	W03947	1.29e-34
13	611	82.8	109	10	W03947	2.48e-34
14	608	82.4	111	19	W03947	2.48e-34
15	608	82.4	111	10	R34277	5.61e-34
16	606	82.1	107	22	W08949	9.16e-34
17	606	82.1	107	10	R54311	1.27e-33
18	605	82.0	107	19	W01269	1.27e-33
19	605	82.0	108	10	R54307	1.50e-33
20	605	82.0	108	19	W01265	1.50e-33

21	604	81.8	107	7	R38593	Human lambda light ch	1.76e-33
22	602	81.4	129	7	R38573	PI05VK-PI05V	2.44e-33
23	602	81.5	129	7	R42866	PI05 rearranged varia	2.44e-33
24	599	81.2	129	7	R38672	W325-JK2	3.99e-33
25	595	80.8	127	22	W09446	Fappa light chain var	4.52e-33
26	594	80.5	107	19	W01266	VL region of HIV neut	9.04e-33
27	594	80.5	107	10	R54308	Anti-HIV gp120 immuno	9.04e-33
28	594	80.5	108	19	W01278	VI region of HIV neut	9.04e-33
29	594	80.5	108	9	R54316	Anti-HIV gp120 immuno	9.04e-33
30	593	80.4	104	9	R54317	Anti-HIV gp120 immuno	1.06e-32
31	593	80.4	104	19	W01279	VL region of HIV neut	1.06e-32
32	591	80.1	109	9	R50217	HSV glycoprotein F bi	1.48e-32
33	590	79.9	107	22	W08948	Kappa light chain var	1.74e-32
34	585	79.3	108	19	W01289	VL region of HIV neut	3.93e-32
35	585	79.3	112	2	R81245	Anti-pseudomonas aera	3.93e-32
36	585	79.3	128	1	R41001	Anti-p aeruginosa st	3.93e-32
37	585	79.3	234	0	R52051	human anti-IgF MAT li	3.93e-32
38	583	79.0	109	9	R50218	HSV glycoprotein F bi	5.45e-32
39	581	78.7	107	5	R52729	Humanised VL region o	7.55e-32
40	578	78.3	109	10	R54563	Anti-HIV gp120 immuno	1.23e-31
41	575	77.9	134	20	W11155	Anti-lung tumour anti	2.01e-31
42	574	77.8	107	7	R37612	hIL2R Ab L chain V re	2.37e-31
43	573	77.6	127	9	R50322	Light chain variable	2.79e-31
44	573	77.6	127	9	R50187	Light chain variable	2.79e-31
45	571	77.4	127	9	R50191	Light chain variable	3.86e-31

## ALIGNMENTS

RESULT 1  
ID R12128 standard; Protein; 349 AA.  
AC R12128:  
DT 01-AUG-1991 (first entry)  
DE 1B1 IgG aberrant light chain with duplicated variable region.  
KW immunoglobulin G; light chain; variable region; duplication;  
KW passive immunity; group B streptococci.  
OS Homo sapiens.

FT Key Location/Qualifiers  
FT Peptide 1..17  
FT /label= leader peptide  
FT Region 18..130  
FT /label= variable region  
FT /note= "L V 1"  
FT Region 131..243  
FT /label= variable region  
FT /note= "L V 2"  
FT Region 244..345  
FT /label= constant region  
FN W09105305-A.  
PD 16-MAY-1991.  
PP 06-NOV-1990; W06426.  
PP 07-NOV-1989; US-432700.  
PA (BRIM ) BRISTOL-MYERS SQUIB.  
DR Shuford WW, Harris LJ, Raff HV;  
DP N-PSB; Q11878.  
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s).  
PT formed by duplicating esp variable region of light chain of IgG class  
PS Example 5, Fig 16, 104pp; English.  
CC This sequence is deduced from the cDNA clone 4B9-VK15 and includes the amino acid sequence beyond the first stop codon. The clone is incomplete, starting from the 5' of the Arg initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across the placenta.  
CC See also Q11879 and Q11880.  
SQ Sequence 349 AA;

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FT /note= "L'V 1" 131..243
FT Region /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
FT W09106305-A.
PN
PD 16-MAY-1991.
PD 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PR (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
PI WPI: 91-163947/22.
DR N-PSDB; Q11878.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 5; Fig 16; 104Pp; English.
CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
CC the amino acid sequence beyond the first stop codon ("x" in the
CC sequence represents a nonsense codon). The clone is incomplete,
CC starting from the G of the ATG initiator codon, but the initial Met
CC is given. Antibody molecules of the invention can include one or two
CC aberrant light chains containing a duplicated variable region, to
CC produce heavier antibodies. These heavier antibodies were found to
CC have higher avidity than antibodies with just a single copy of the
CC L'V region. The antibodies can be used to treat disease, e.g.
CC infection by Streptococcus agalactiae. They are able to pass across
CC the placenta.
CC See also Q11879 and Q11880.
CC Sequence 414 AA:
SQ

Query Match 87.9%; Score 649; DB 2; Length 414.
Best Local Similarity 89.6%; Pred. No. 1,11e-36;
Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps

Db 24 ltqspatlslsgperatiscrasgsvgsylawygqkpgqaprpilvdasnratgiparfs 83
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QY 3 LTQSPATLSLSPGERATISCTPASQSVNKYLAWYQCKPGQAPPIILYDASNPATGIPAPFS 62

Db 84 gsgsgtdftltisslepedfavyycqhrdwpggaatfggatkveik 129
|||||
QY 63 GSGSGTDFLTISNLEPEDFAVYVCQQRSDW---VTFSGGTRKVEIK 105

RESULT 4
ID R13111 standard; Protein; 414 AA.
AC R13111;
DT 10-MAR-1993 (revised)
DT 01-AUG-1991 (first entry)
DE 1B1 IgG aberrant light chain with duplicated variable region.
DE Immunoglobulin G; light chain; variable region; duplication;
DE passive immunity; group B streptococci.
DE Homo sapiens.
FS Key Location/Qualifiers
FT Peptide 1..17
FT /label= leader
FT Region 18..130
FT /label= variable region
FT /note= "L'V 1" 131..243
FT Region /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
PN W09106305-A.
PD 16-MAY-1991.
PD 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PR (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
PI WPI: 91-163947/22.
DR N-PSDB; Q11878.

```

PT \*Oligomeric immunoglobulin(s) with high avidity for antigen(s) -  
 PT formed by duplicating esp. variable region of light chain of IgG  
 PT class  
 PS Example 5; Fig 16; 104pp; English.  
 CC This sequence is deduced from the cDNA clone 4R9-Vk15 and includes  
 CC the amino acid sequence beyond the first stop codon ("x" in the  
 CC sequence represents a nonsense codon). The clone is incomplete,  
 CC starting from the G of the ATG initiator codon, but the initial Met  
 CC is given. Antibody molecules of the invention can include one or two  
 CC aberrant light chains containing a duplicated variable region, to  
 CC produce heavier antibodies. These heavier antibodies were found to  
 CC have higher avidity than antibodies with just a single copy of the  
 CC L/V region. The antibodies can be used to treat disease, e.g.  
 CC infection by Streptococcus atalactiae. They are able to pass across  
 CC the placenta.  
 CC See also Q11879 and Q11880.  
 SQ Sequence 414 AA;

Query Match 87.9%; Score 649; DB 2; Length 414;  
 Best Local Similarity 89.6%; Pred No. 1,11e-36;  
 Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps 1;  
 Db 24 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 83  
 QY 3 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 62  
 Db 84 qsgqtdftltisslepedfavyvycqrshw 129  
 QY 63 GSGSGTDTLTISNLEPEDFAVYVYCCQQRSDW---VTEGGGKVEIK 105

RESULT 5  
 ID R38648 standard; Protein: 115 AA.  
 AC R38648;  
 DT 10-NOV-1993 (first entry)  
 DE Human V-kappa fragment encoded by clone vk65.3.  
 KW Immunoglobulin; light chain variable region; minilocus;  
 KW isotype switching; unrearranged functional V $\kappa$  gene segment;  
 KW human light chain transgene.  
 OS Homo sapiens.  
 PN WO9112227-A.  
 PD 24-JUN-1993.  
 PF 17-DEC-1992; U10983.  
 PR 17-DEC-1991; US-810279.  
 PR 18-MAR-1992; US-853408.  
 PR 23-JUN-1992; US-904068.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N.  
 DR N-PSDB; Q44222.  
 DR Transgenic non-human animals contg. immunoglobulin heavy chain  
 PT trans gene - used to produce useful antibodies by isotype  
 PT switching  
 PS Example 21; Fig 41; 196pp; English.  
 CC The V-kappa specific oligonucleotide Q50327 was used to probe a  
 CC human placental genomic DNA library cloned into lambdaEMBL3/SB6/77  
 CC DNA fragments containing V-kappa segments from positive phage  
 CC clones were subcloned into plasmid vectors. Variable gene segments  
 CC from the resulting clones were sequenced and functional clones were  
 CC selected on the basis of open reading frames, intact donor and  
 CC acceptor splice sites and intact recombination sequences. The  
 CC sequences obtained from four different plasmid clones were  
 CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q4425,  
 CC respectively) and the amino acid sequences of the V-kappa regions  
 CC they encode were deduced.  
 SQ Sequence 115 AA;

Query Match 84.8%; Score 626; DB 7; Length 115;  
 Best Local Similarity 95.6%; Pred No. 4.82e-35;  
 Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 83  
 QY 3 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 62

QY 3 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 62  
 Db 84 qsgqtdftltisslepedfavyvycqrshw 114  
 QY 63 GSGSGTDTLTISNLEPEDFAVYVYCCQQRSDW 93

RESULT 6  
 ID R62928 standard; Protein: 115 AA.  
 AC R62928;  
 DT 07-JUN-1995 (first entry)  
 DE Human V-kappa vk65.3 region.  
 KW Transgenic mouse; transgenic animal; antibody engineering;  
 KW variable region; light chain; minilocus transgene;  
 KW chimeric antibody.  
 OS Homo sapiens.  
 PN WO9425585-A.  
 PD 10-NOV-1994.  
 PF 25-APR-1994; U04580.  
 PR 26-APR-1993; US-053131.  
 PR 22-JUL-1993; US-096762.  
 PR 18-NOV-1993; US-155301.  
 PR 03-DEC-1993; US-161739.  
 PR 10-DEC-1993; US-165699.  
 PR 09-MAR-1994; US-209741.  
 PA (GENP-) GENPHARM INT INC.  
 PI Kay RM, Lonberg N.  
 DR WPI; 94-358263/44.  
 DR N-PSDB; Q78852.  
 DR Transgenic non-human animals producing heterologous or chimeric  
 PT antibodies - for binding a pre-determined human antigen with  
 PT increased affinity  
 PS Disclosure; Fig. 41; 296pp; English.  
 CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in  
 CC Q78852-Q78855, respectively) each contain a V-kappa gene segment  
 CC that can be used to form a complete human light chain minilocus  
 CC transgene for expression in a nonhuman transgenic animal for  
 CC heterologous antibody production. The deduced amino acid  
 CC sequences of the V-kappa coding regions are given in R62928 R62931.  
 SQ Sequence 115 AA;

Query Match 84.8%; Score 626; DB 11; Length 115;  
 Best Local Similarity 95.6%; Pred. No. 4.82e-35;  
 Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 83  
 QY 3 ltqspatlsppgeratiscrasqsvsylvayqgkqgqprllydasratgiparfs 62  
 Db 84 qsgqtdftltisslepedfavyvycqrshw 114  
 QY 63 GSGSGTDTLTISNLEPEDFAVYVYCCQQRSDW 93

RESULT 7  
 ID W03946 standard; Protein: 120 AA.  
 AC W03946;  
 DT 14-APR-1997 (first entry)  
 DE DNA fragment vk65.3 variable kappa chain protein product.  
 KW Variable; kappa chain; gene segment; human; RNA fragment; vk65.3;  
 KW unrearranged; light chain; minilocus; transgene; transgenic; mouse;  
 KW production; heterologous; antibody, gamma; immunoglobulin.  
 OS Homo sapiens.  
 PN US5545806-A.  
 PD 13-AUG-1996.  
 PF 29-AUG-1990; 574748.  
 PR 29-AUG-1990; US-574748.  
 PR 31-AUG-1990; US-575962.  
 PR 17-DEC-1991; US-810279.  
 PR 18-MAR-1992; US-853408.  
 PR 23-JUN-1992; US-904068.  
 PR 16-DEC-1992; US-908650.  
 PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;  
DR WPI: 96-383736/38;  
DR N-PSDB: T37180.

PT Prodn. of heterologous human immunoglobulin(s) - by immunising  
PT transgenic mice

PS Example 21: Fig 41: 94pp; English.

CC The present sequence is the protein product of the variable kappa  
CC chain gene segment containing human DNA fragment, vk65.3, which  
CC was co-injected along with the human DNA fragments vk65.5, vk65.8  
CC and vk65.15 into half day mouse embryo pronuclei, to generate an  
CC unrearranged light chain minilocus transgene. The resulting  
CC transgenic mice can be used for the production of heterologous  
CC (i.e. human) antibodies against specific antigens, this comprises  
CC immunising a mouse with a preselected antigen and collecting  
CC antigen binding heterologous human gamma immunoglobulins.  
SQ Sequence 120 AA;

Query Match 84.8%; Score 626; DB 20; Length 120;  
Best Local Similarity 95.6%; Pred. No. 4 82e-35;  
Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 29 ltqspatlslpgeratlscrasqvssylawyqkpgqaprllydasnratgiparifs 88

QY 3 LTQSPATLSLSPGERATLSQSPASQSVNKYLAWYQKPGQAPRLIYDASNRPATGIPARFS 62

Db 89 gsgsgtdftltisslepedfavyycqrsnw 119

QY 63 GSGSGTDFTLTISNLEPEDFAVYCYQQRSDW 93

#### RESULT 8

ID R38649 standard; Protein; 115 AA

AC R38649;

DE Human V-kappa fragment encoded by clone vk65.5.

KW Immunoglobulin; light chain variable region; minilocus;

KW isotype switching; unrearranged functional V $\kappa$  gene segment;

OS Homo sapiens.

PN W0931227-A.

PD 24-JUN-1993.

PF 17-DEC-1992; U10983.

PR 17-DEC-1991; US-810279.

PR 18-MAR-1992; US-853408.

PR 23-JUN-1992; US-904068.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;

DR WPI: 93-214169/26.

DR N-PSDB: Q44223.

PT Transgenic non-human animals contg. immunoglobulin heavy chain

PT trans gene - used to produce useful antibodies by isotype

PT switching

PS Example 21: Fig 42: 196pp; English.

CC The V-kappa specific oligonucleotide Q50327 was used to probe a

CC human placental genomic DNA library cloned into lambdaEMBL3/SP6/T7.

CC DNA fragments containing V-kappa segments from positive phage

CC clones were subcloned into plasmid vectors. Variable gene segments

CC from the resulting clones were sequenced and functional clones were

CC selected on the basis of open reading frames, intact donor and

CC acceptor splice sites and intact recombination sequences. The

CC sequences obtained from four different plasmid clones were

CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,

CC respectively) and the amino acid sequences of the V-kappa regions

CC they encode were deduced.

CC Sequence 115 AA;

#### Query Match

Best Local Similarity 84.0%; Score 620; DB 7; Length 115;

Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlslpgeratlscrasqvssylawyqkpgqaprllydasnratgiparifs 83

QY 3 LTQSPATLSLSPGERATLSQSPASQSVNKYLAWYQKPGQAPRLIYDASNRPATGIPARFS 62

Db 84 gsgsgtdftltisslepedfavyycqrsnw 114

QY 63 GSGSGTDFTLTISNLEPEDFAVYCYQQRSDW 93

#### RESULT 9

ID R62929 standard; Protein; 115 AA.

AC R62929;

DE Human V-kappa vk65.5 region.

KW Transgenic mouse; transgenic animal; antibody engineering;

KW variable region; light chain; minilocus transgene;

KW chimeric antibody.

OS Homo sapiens.

PN W09425585-A.

PD 10-NOV-1994.

PF 25-APR-1994; U04580.

PP 26-APR-1993; US-053131.

PR 22-JUL-1993; US-096762.

PR 18-NOV-1993; US-155301.

PR 03-DEC-1993; US-161739.

PR 10-DEC-1993; US-165699.

PP 09-MAR-1994; US-209741.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;

DR WPI: 94-359263/44.

DR N-PSDB: Q78853.

PT Transgenic non-human animals producing heterologous or chimeric

PT antibodies - for binding a pre-determined human antigen with

PT increased affinity

PS Disclosure: Fig 42: 246pp; English

CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in

CC Q78852-Q78855, respectively) each contain a V-kappa gene segment

CC that can be used to form a complete human light chain minilocus

CC transgene for expression in a nonhuman transgenic animal for

CC heterologous antibody production. The deduced amino acid

CC sequences of the V-kappa coding regions are given in P62928-P62931.

SQ Sequence 115 AA;

Query Match 84.0%; Score 620; DB 11; Length 115;

Best Local Similarity 93.4%; Pred. No. 1.29e-34;

Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlslpgeratlscrasqvssylawyqkpgqaprllydasnratgiparifs 83

QY 3 LTQSPATLSLSPGERATLSQSPASQSVNKYLAWYQKPGQAPRLIYDASNRPATGIPARFS 62

Db 84 gsgsgtdftltisslepedfavyycqrsnw 114

QY 63 GSGSGTDFTLTISNLEPEDFAVYCYQQRSDW 93

#### RESULT 10

ID W03947 standard; Protein; 115 AA.

AC W03947;

DE DNA fragment vk65.5, variable kappa chain protein product.

KW Variable; kappa chain; gene segment; human; DNA fragment; vk65.5;

KW unrearranged; light chain; minilocus; transgene; transgenic; mouse;

KW production; heterologous; antibody; gamma; immunoglobulin.

OS Homo sapiens.

PN US5545806-A.

PD 13-AUG-1996.

PF 29-AUG-1990; 574748.

PR 29-AUG-1990; US-574748.

PR 31-AUG-1990; US-575962.

PR 17-DEC-1991; US-810279.

PR 18-MAR-1992; US-853408.

PR 23-JUN-1992; US-904068.

PR 16-DEC-1992; US-900860.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;



DR \*WPI: 96-383736/38.  
 DR N-PSDB: T37181.  
 PT Prodn. of heterologous human immunoglobulin(s) - by immunising  
 PT transgenic mice  
 PS Example 21; Fig 42; 94pp; English.  
 CC The present sequence is the protein product of the variable kappa  
 CC chain gene segment containing human DNA fragment, vk65.5, which  
 CC was co-injected along with the human DNA fragments vk65.3, vk65.8  
 CC and vk65.15 into half day mouse embryo pronuclei, to generate an  
 CC unrearranged light chain minilocus transgene. The resulting  
 CC transgenic mice can be used for the production of heterologous  
 CC (i.e. human) antibodies against specific antigens, this comprises  
 CC immunising a mouse with a preselected antigen and collecting  
 CC antigen binding heterologous human gamma immunoglobulins.  
 SQ Sequence 115 AA;

Query Match 84.0%; Score 620; DB 20; Length 115;  
 Best Local Similarity 93.4%; Pred. No. 1.29e-34;  
 Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlslegratlsrscasqgvsnylawyqkpgqaprllydasnratgiparfs 83  
 QY 3 ltqspatlslegratlsrscasqgvsnylawyqkpgqaprllydasnratgiparfs 52  
 Db 84 gsgqtdftltisrlepedfavyycqgrsnw 114  
 QY 63 GSGSGTDFLTISNLEPEDFAVYVCQQRSDW 93

RESULT 11  
 ID R54275 standard; protein: 109 AA  
 AC R54275;  
 DT 10-NOV-1994 (first entry)  
 DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.  
 KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;  
 KW neutralisation; monoclonal antibody; light chain; variable region;  
 KW framework region; complementarity determining region.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 1...23  
 FT /label= FR1  
 FT Region 24...35  
 FT /label= CDR1  
 FT Region 36...50  
 FT /label= FR2  
 FT Region 51...57  
 FT /label= CDR2  
 FT Region 58...89  
 FT /label= FR3  
 FT Region 90...97  
 FT /label= CDR3  
 FT Region 98...109  
 FT /label= FR4  
 PN W09407922-A.  
 PD 14-APR-1994.  
 PF 30-SEP-1993; U09328.  
 PR 30-SEP-1992; US-954148.  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI: 94-135516/16.  
 PT New human monoclonal antibodies neutralising HIV - react with  
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
 PT or in vitro diagnosis and for passive immuno-therapy  
 PS Claim 11; Page 215-216; 248pp; English.  
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
 CC amplification using primers specific for heavy and light chain  
 CC variable regions. The amplification products were inserted into a  
 CC dicistronic vector to produce a library of fragments. E.coli XL1  
 CC Blue cells were transformed with the library. Filamentous phage were  
 CC produced which expressed the MAB regions on their surface. Panning  
 CC with gp120 and gp41 resulted in the recovery of immunoreactive  
 CC clones. The light chain VL region sequence R54275 neutralises HIV1  
 CC gp41.

SQ Sequence 109 AA;  
 Query Match 83.5%; Score 616; DB 19; Length 109;  
 Best Local Similarity 84.9%; Pred. No. 2.48e-34;  
 Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Db 2 aeltqspatlslegratlsrscasqgvsnylawyqkpgqaprllydasnratgipd 61  
 QY 1 aeltqspatlslegratlsrscasqgvsnylawyqkpgqaprllydasnratgipd 59  
 Db 62 rfsqsgtdftltisrlepedfavyycqgsgsfgggtkveik 107  
 QY 60 RFSGSGTDFLTISNLEPEDFAVYVCQQRSDWVTFGGGKVEIK 105

RESULT 12  
 ID W01320 standard; protein: 109 AA.  
 AC W01320;  
 DT 29-JAN-1997 (first entry)  
 DE VL of Fab, DL 41 19, binds to HIV gp41.  
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;  
 KW MAB; HIV, human immunodeficiency virus; glycoprotein, gp120; clone;  
 KW virus infectivity assay; precursor gp160; immunocompetence; human;  
 KW anti-HIV antibody; detection; HIV infection.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 1 23  
 FT /label= FR1  
 FT Region 24...35  
 FT /label= CDR1  
 FT Region 36...50  
 FT /label= FR2  
 FT Region 51...57  
 FT /label= CDR2  
 FT Region 58...89  
 FT /label= FR3  
 FT Region 90...97  
 FT /label= CDR3  
 FT Region 98...109  
 FT /label= FR4  
 PN W09602273-A1.  
 PD 01-FEB-1996.  
 PF 11-JUL-1995; U08743.  
 PR 18-JUL-1994; US-276852.  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI: 96-179601/18.  
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in  
 PT passive immuno-therapy and detection of HIV infection.  
 PS Example 3; Fig 19; 366pp; English.  
 CC The sequences given in W01320-24 represent the light chain variable  
 CC regions (VH) of a series of antibody fragments (FAB's) which are  
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents  
 CC the sequence of the clone, DL 41 19. These sequences represent light  
 CC chains which bind to the heavy light chain clones given in W01315-19. A  
 CC monoclonal antibody containing one of these Fab sequences may have the  
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity  
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.  
 CC The MAB may be used for determining immunocompetence of a human anti-HIV  
 CC antibody and in the detection of HIV infection.  
 SQ Sequence 109 AA;

Query Match 83.5%; Score 616; DB 19; Length 109;  
 Best Local Similarity 84.9%; Pred. No. 2.48e-34;  
 Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Db 2 aeltqspatlslegratlsrscasqgvsnylawyqkpgqaprllydasnratgipd 61  
 QY 1 aeltqspatlslegratlsrscasqgvsnylawyqkpgqaprllydasnratgipd 59  
 Db 62 rfsqsgtdftltisrlepedfavyycqgsgsfgggtkveik 107  
 QY 60 RFSGSGTDFLTISNLEPEDFAVYVCQQRSDWVTFGGGKVEIK 105

```

RESULT 13
ID R56286 standard; Protein: 109 AA
AC R56286;
DT 04-MAR-1995 (first entry)
DE Light chain of Amb al-specific IgG4 antibody.
KW Allergen-specific immunoglobulin A; IgA; AL 15-5.2; light chain;
KW Allergen Amb a 1; ragweed; Ambrosia elator.
OS Synthetic.
PN W09414475-A.
PD 07-JUL-1994.
PP 20-DEC-1993; U12501.
PR 21-DEC-1992; US-994126.
PA (TANO-) TANOX BIOSYSTEMS INC.
PI Chang TW;
DR WPI: 94-234353/28.
DR N-PSDB; Q66538.
PT Compsn. contg. allergen specific IgA for treating mucosal tissue
PT - and conjugates of allergen specific Ig with polymer, for
PT treating IgE mediated allergies and for isolation of specific
PT allergens
PS Example; Page 27-28; 36pp; English.
CC Blood samples were collected from patients immunised with allergens
CC including ragweed (Ambrosia elator) extracts. The dominant allergen
CC in short ragweed is Amb a 1. Purified PBIs were immortalised and
CC then fused with mouse myeloma cell line 653 and the resultant clones
CC were screened using Amb a 1 protein. A single cell subclone AL 16-5.2,
CC secreting Amb al-specific IgG4, kappa antibody was selected. Total
CC RNA was prep'd. from the AL 16-5.2 cells and first strand cDNA was
CC pred. using oligo dt primers. When the first strand cDNA was used as
CC the template, and the 5' and 3' kappa light chain primers (Q66540,
CC Q66541) were used in PCR and amplified band of the expected size was
CC noted. The DNA sequence of several subclones contg. this amplified
CC DNA fragment was determined. The sequence and its deduced AA
CC sequence are shown in Q66538 and R56286. Comparison of the deduced
CC AL 16-5.2 L-chain sequence with human V region sequences indicates
CC that it is a member of the human VK III subgp.
SQ Sequence 109 AA;

Query Match 82.8%; Score 611; DB 10; Length 109.
Best Local Similarity 82.1%; Pred No. 5 61e-34;
Matches 87; Conservative 10; Mismatches 5; Indels 4; Gaps 4,

Db 4 ltsgpqtllslspgeratlsrsgatvsngylawyqkpgqaprllyvgastatdipd 63
QY 3 LTQSPATLSLSPGERATLSRSGATVSNGK-YLAWYQKPGQAPRLLYVDASNPAIGIPARF 61

Db 64 tsgsgtdftltisrlepdefavyyccqfrnsqw-tfgggtkveik 108
QY 62 SGSGSGTDFTLTISNLEPDEFVAVYCCQ-R-SDWVTFGGGTKEIK 105

RESULT 14
ID W01322 standard; Protein: 111 AA.
AC W01322;
DT 29-JAN-1997 (first entry)
DE VL of Fab, GL 41 1, binds to HIV gp41.
KW Heavy chain, light chain, variable region, VH, monoclonal antibody,
KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW Virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1 23
FT /label= FR1
FT Region 24...35
FT /label= CDR1
FT Region 36...50
FT /label= FR2
FT Region 51...57
FT /label= CDR2
FT Region 58...89
FT /label= FR3
FT Region 90 97
FT /label= CDR3
FT Region 98...111
FT /label= FR4
FN W09407922-A.
PD 14-APR-1994.
PP 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo

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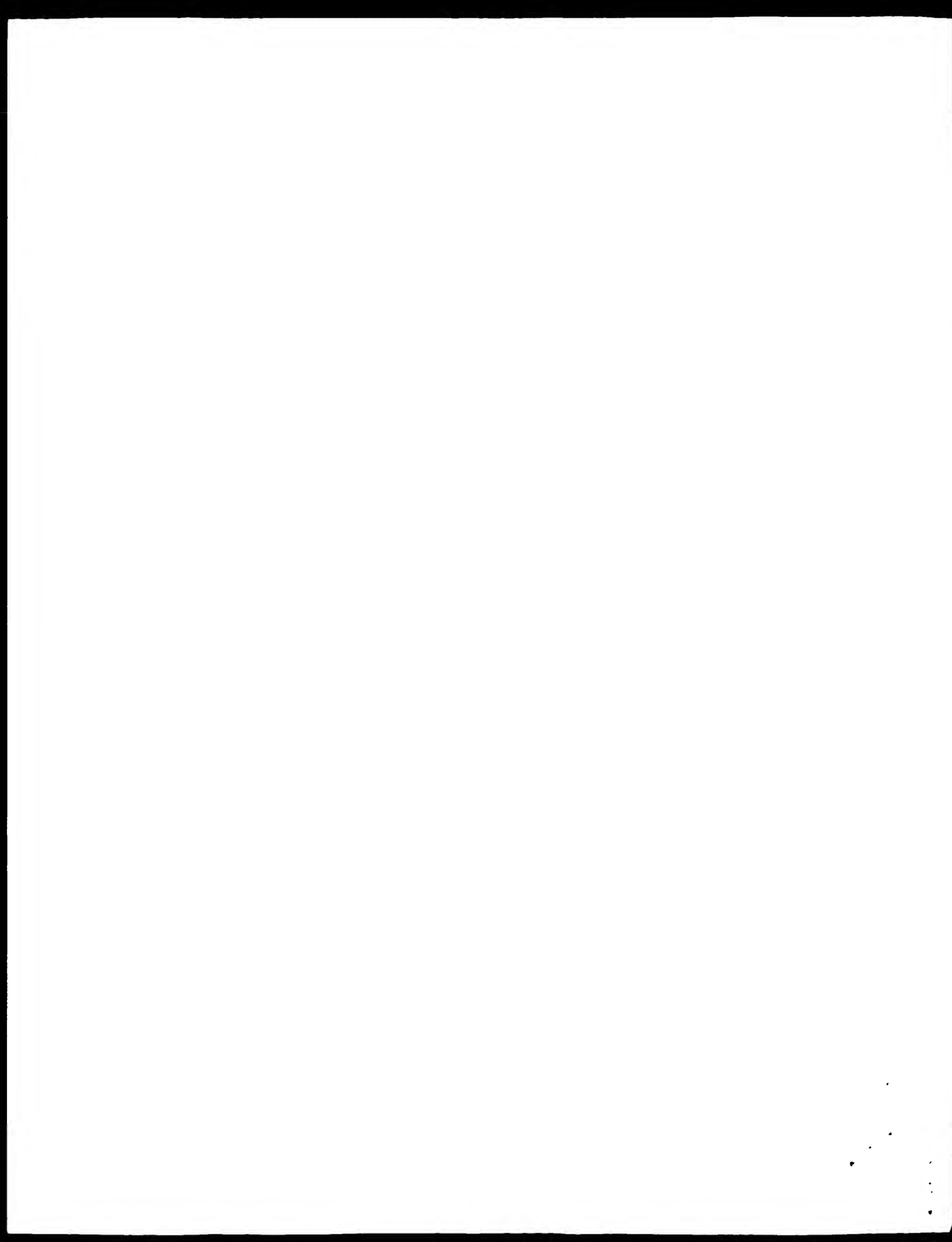
PT or in vitro diagnosis and for passive immuno-therapy  
PS Claim 11: Page 217: 248pp: English.  
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
CC amplification using primers specific for heavy and light chain  
CC variable regions. The amplification products were inserted into a  
CC dicistronic vector to produce a library of fragments. E.coli XL1  
CC Blue cells were transformed with the library. Filamentous phage were  
CC produced which expressed the MAB regions on their surface. Panning  
CC with gp120 and gp41 resulted in the recovery of immunoreactive  
CC clones. The light chain VL region sequence R54277 neutralises HIV1  
CC gp41.  
SQ Sequence 111 AA:

Query Match 82.4%; Score 608; DB 10; Length 111;  
Best Local Similarity 83.0%; Pred. No. 9.16e-34;  
Matches 88; Conservative 7; Mismatches 10; Indels 1; Gaps 1:

Db 2 aeltspqtislsperatlsrasqvsngylawyqkpcqaprllygastratdipd 61  
QY 1 AELTQSPATLSLSPGEPATLSPPASQVSNK-YLAWYQKPCQAPRLLIYDASNPATGIPA 59

Db 62 rfsgsqsgadflalsrlepedfavyccqyagshftqggtkleik 107  
QY 60 RFSGSGGIDFTLIISNLEPEDFAVYCCQPSDWVTFGGTKVEIK 105

Search completed: Tue Feb 24 07:20:37 1998  
Job time : 30 secs.



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(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:17:10 1998; Maspar time 4.91 Seconds  
Tabular output not generated. 462.245 Million cell updates/sec  
Title: >US-08-844-215-8  
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Perfect Score: 752  
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Scoring table: PAM 150  
Gap 11  
Searched: 59021 seqs, 21210388 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11  
Statistics: Mean 40.565 Variance 71.086; scale 0.571

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description Pred. No.
1	712	93.4	129 5 KV3M_HUMAN IG KAPPA CHAIN PRECUR 7.40e-136
2	701	92.0	129 5 KV3L_HUMAN IG KAPPA CHAIN PRECUR 2.79e-133
3	585	89.9	104 5 KV3R_HUMAN IG KAPPA CHAIN V-III 1.55e-129
4	585	89.9	104 5 KV3E_HUMAN IG KAPPA CHAIN V-III 1.55e-129
5	674	109.5	104 5 KV3D_HUMAN IG KAPPA CHAIN V-III 5.76e-127
6	671	88.1	109 5 KV3A_HUMAN IG KAPPA CHAIN V-III 3.13e-123
7	658	86.4	108 5 KV3G_HUMAN IG KAPPA CHAIN V-III 2.45e-118
8	637	83.6	129 5 KV3H_HUMAN IG KAPPA CHAIN PRECUR 7.40e-136
9	622	81.6	100 5 KV3C_HUMAN IG KAPPA CHAIN PRECUR 2.79e-133
10	611	80.2	128 5 KV3F_HUMAN IG KAPPA CHAIN PRECUR 7.40e-136
11	605	79.4	109 5 KV3I_HUMAN IG KAPPA CHAIN V-III 5.69e-111
12	560	73.5	115 5 KV3J_HUMAN IG KAPPA CHAIN PRECUR 1.72e-100
13	558	73.2	115 5 KV3L_HUMAN IG KAPPA CHAIN PRECUR 4.99e-100
14	537	70.5	108 5 KV3M_HUMAN IG KAPPA CHAIN V-I RE 3.42e-95
15	528	69.3	108 5 KV3R_HUMAN IG KAPPA CHAIN V-I RE 4.01e-93
16	524	68.8	134 5 KV3E_HUMAN IG KAPPA CHAIN PRECUR 3.32e-92
17	523	68.6	104 5 KV3D_HUMAN IG KAPPA CHAIN V-I RE 5.44e-92
18	518	68.0	107 5 KV3I_HUMAN IG KAPPA CHAIN V-I RE 7.91e-91
19	518	68.0	104 5 KV3J_HUMAN IG KAPPA CHAIN V-I RE 7.91e-91
20	518	68.0	108 5 KV3H_HUMAN IG KAPPA CHAIN V-I RE 7.91e-91
21	515	67.7	108 5 KV3G_HUMAN IG KAPPA CHAIN V-I RE 2.27e-90
22	512	67.2	108 5 KV3F_HUMAN IG KAPPA CHAIN V-I RE 1.88e-89

23	510	66.9	108 5 KV1Y_HUMAN IG KAPPA CHAIN V-I RE 5.35e-89
24	509	66.8	108 5 KV1V_HUMAN IG KAPPA CHAIN V-I RE 9.13e-89
25	502	55.9	114 5 KV4A_HUMAN IG KAPPA CHAIN V-IV RE 3.45e-87
26	501	65.7	108 5 KV1L_HUMAN IG KAPPA CHAIN V-I RE 6.19e-87
27	498	65.4	129 5 KV1W_HUMAN IG KAPPA CHAIN PRECUR 3.00e-86
28	496	65.1	108 5 KV1O_HUMAN IG KAPPA CHAIN V-I RE 8.60e-86
29	492	64.6	133 5 KV4B_HUMAN IG KAPPA CHAIN PRECUR 7.05e-85
30	488	64.0	108 5 KV1E_HUMAN IG KAPPA CHAIN V-I RE 5.77e-84
31	486	63.8	108 5 KV1G_HUMAN IG KAPPA CHAIN V-I RE 1.55e-83
32	483	63.4	129 5 KV1X_HUMAN IG KAPPA CHAIN PRECUR 7.98e-83
33	482	63.3	108 5 KV1P_HUMAN IG KAPPA CHAIN V-I RE 1.35e-82
34	482	63.3	133 5 KV2F_HUMAN IG KAPPA CHAIN PRECUR 1.35e-82
35	480	63.0	108 5 KV1O_HUMAN IG KAPPA CHAIN V-I RE 3.85e-82
36	480	63.0	109 5 KV1T_HUMAN IG KAPPA CHAIN V-I RE 3.85e-82
37	479	62.9	111 5 KV4O_MOUSE IG KAPPA CHAIN V-III 6.51e-82
38	476	62.5	108 5 KV1A_HUMAN IG KAPPA CHAIN V-I RE 3.14e-81
39	476	62.5	108 5 KV1S_HUMAN IG KAPPA CHAIN V-I RE 3.14e-81
40	476	62.5	117 5 KV1J_HUMAN IG KAPPA CHAIN PRECUR 3.14e-81
41	475	62.3	112 5 KV3G_MOUSE IG KAPPA CHAIN V-III 5.30e-81
42	471	61.8	108 5 KV1C_HUMAN IG KAPPA CHAIN V-I RE 4.31e-80
43	469	61.5	108 5 KV5J_MOUSE IG KAPPA CHAIN V-V RE 1.23e-79
44	469	61.5	111 5 KV3Q_MOUSE IG KAPPA CHAIN V-III 1.23e-79
45	469	61.5	131 5 KV3I_MOUSE IG KAPPA CHAIN PRECUR 1.23e-79

ALIGNMENTS

RESULT 1  
ID KV3M\_HUMAN STANDARD: PRT: 129 AA.  
AC P18136;  
DI 01-NOV-1990 (REL. 16, CREATED)  
DI 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
DI 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VEPTERATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 88171307.  
PA KIPES T. J., TOMHAVE F., CHEN P. P., CAPSON D. A.:  
RL J. EXP. MED. 167:840-852(1988).  
CC -DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCTIC  
CC LEUKEMIA.  
DR PIR: P10021; K3HUH1.  
DR HSSP: P01607; 1DFB.  
KW IMMUNOGLOBULIN V REGION; SIGNAL.  
FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).  
FT DOMAIN 21 43 FRAMEWORK 1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 56 70 FRAMEWORK 2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 78 109 FRAMEWORK 3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 119 129 JK1 SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA: 14070 MW: 35000369 CRC32.  
Query Match 93.4%; Score 712; DB 5; Length 129;  
Best Local Similarity 94.3%; Pred. No. 7.40e-136;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Db 24 lcsqstslsperatlsrassqsvssylawgqkpgqaprllycassratidprf 83  
QY 3 lcsqstslsperatlsrassqsvssylawgqkpgqaprllycassratidprf 62  
Db 84 sqsgsqtddftlsrlslepxdfavyyccgqgsspwtfqgkveik 128  
QY 63 sqsgsqtddftlsrlslepxdfavyyccgqgsspwtfqgkveik 107

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RESULT 2
ID KV3L_HUMAN STANDARD: PRT: 129 AA.
AC P18135;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAH).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DE PIR: P18022; K3HUHA.
DR HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14073 MW: 2044885E CRC32:

Query Match 92.0%; Score 701; DB 5; Length 129;
Best Local Similarity 94.3%; Pred. No. 2.79e-133;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltqspgtlslspgeratlscrasqsvssylawyqkqpgqaprllygassratgipdrf 83
QY 3 LTQSPGTLSPGERATLSGRASQSVSSNYLAWYQQRPGQAPRLLYGASSRATGIPDRF 62
|||||
Db 84 sqsgsgtdftltisrlepedfavyycqygsprtfqgqkveik 128
QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGQTKVEIK 107
|||||

RESULT 3
ID KV3B_HUMAN STANDARD: PRT: 109 AA.
AC P01620;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPPA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DE PIR: A01892; K3HUSI.
DR HSSP: P01607; 1DPB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11775 MW: 60850D5D CRC32:

Query Match 89.9%; Score 685; DB 5; Length 109;

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Best Local Similarity 91.4%; Pred. No. 1.55e-129;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspgtlslspgeratlscrasqsvssylawyqkqpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSGRASQSVSSNYLAWYQQRPGQAPRLLYGASSRATGIPDRF 62
|||||
Db 64 sqsgsgtdftltisrlepedfavyycqygsprtfqgqkveik 108
QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGQTKVEIK 107
|||||

RESULT 4
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01623;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPPA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DE PIR: A01896; K3HUMI.
DR HSSP: P01607; 1DPB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11746 MW: 7D8F5D75 CRC32:

Query Match 89.9%; Score 685; DB 5; Length 109;
Best Local Similarity 92.4%; Pred. No. 1.55e-129;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltqspgtlslspgeratlscrasqsvssylawyqkqpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSGRASQSVSSNYLAWYQQRPGQAPRLLYGASSRATGIPDRF 62
|||||
Db 64 sqsgsgtdftltisrlepedfavyycqygsprtfqgqkveik 108
QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGQTKVEIK 107
|||||

RESULT 5
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01622;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TI).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 72188439.
RA SUTER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.;
PL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
CC -!- THIS C REGION OF THIS CHAIN HAS THE INV (3) MAPKRP.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DE PIR: A01895; K3HUTI.
DR HSSP: P01607; 2IMM.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11789 MW: D03795B1 CRC32:

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Query Match 88.5%; Score 674; DB 5; Length 109;  
 Best Local Similarity 90.5%; Pred No. 5,76e-127;  
 Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltsqptslsppgeratlsralscrasqsvsnflawyqkpgqgprlllyvassratgipdrf 63

QY 3 LTQSPGTLISLSPGERATLSRALSQSVSSNYLAWYQKPGQGPRLLYVASSRATGIPDRF 62

Db 64 ssgsgtdftltisrlepedfavyycqygsspsstfaggtkveik 108

QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRMTFGGTKEIK 107

RESULT 6

ID KV3C\_HUMAN STANDARD: PRT: 108 AA

AC P04206;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-III REGION (R6)

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES;

RN [1]

RP SEQUENCE.

RA MILSTEIN C.;

PL FERBS LETT. 2:301-304(1969).

CC -1- THIS IS A BENCE-JONES PROTEIN

DR PIR: A01891; K3HUG6.

DR HSSP: P01607; IMCP.

KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.

FT DISULFID 23 89

FT NON\_TER 108 108

SQ SEQUENCE 108 AA; 11635 MW; 46D6B68E CRC32;

Query Match 88.1%; Score 671; DB 5; Length 108;

Best Local Similarity 84.8%; Pred No. 2.89e-126;

Matches 89; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltsqptslsppgeratlsralscrasqsvsnflawyqkpgqgprlllyvassratgipdrf 63

QY 3 LTQSPGTLISLSPGERATLSRALSQSVSSNYLAWYQKPGQGPRLLYVASSRATGIPDRF 62

Db 64 ssgsgtdftltisrlepedfavyycqygsspsstfaggtkveik 108

QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRMTFGGTKEIK 107

RESULT 7

ID KV3C\_HUMAN STANDARD: PRT: 108 AA

AC P04206;

DT 20-MAR-1987 (REL. 04, CREATED)

DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)

DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-III REGION (R6)

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES;

RN [1]

RP SEQUENCE.

RA NEWKIRK M.; CHEN P.P.; CARSON D.A.; POSNETT D.; CAPPA J.D.

PL MOL IMMUNOL. 23:238-244(1986)

DR PIR: A01893; K3HUG6.

DR HSSP: P01607; 1CEB.

KW IMMUNOGLOBULIN V REGION

FT DISULFID 23 89

FT NON\_TER 109 109

SQ SEQUENCE 109 AA; 11830 MW; 893DCC4A CRC32;

Query Match 86.4%; Score 658; DB 5; Length 109;

Best Local Similarity 87.6%; Pred No. 3.13e-123;

Matches 92; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 4 ltsqptslsppgeratlsralscrasqsvsnflawyqkpgqgprlllyvassratgipdrf 63

QY 3 LTQSPGTLISLSPGERATLSRALSQSVSSNYLAWYQKPGQGPRLLYVASSRATGIPDRF 62

Db 64 ssgsgtdftltisrlepedfavyycqygsspsstfaggtkveik 108

QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRMTFGGTKEIK 107

RESULT 8

ID KV3C\_HUMAN STANDARD: PRT: 129 AA

AC P04207;

DT 20-MAR-1987 (REL. 04, CREATED)

DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN PRECURSOR V-III REGION (C1D) (RHEUMATOID FACTOR).

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 86177570.

RA JIRIK F.P.; SORGE J.; FONG S.; HEITZMANN J.G.; CURD J.G.; CHEN P.P.

PL GOLDFIEB P.; CARSON D.A.;

PL PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2199(1986).

DR EMBL: M12740; G553486;

DR PIR: A01898; K3HUG1.

DR HSSP: P01607; IAAG.

KW IMMUNOGLOBULIN V REGION: SIGNAL.

FT SIGNAL 1 20

FT CHAIN 21 129

FT DOMAIN 21 43

FT DOMAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 44 54

FT DOMAIN 55 59

FT DOMAIN 55 59

FT DOMAIN 70 76

FT DOMAIN 70 76

FT DOMAIN 109 118

FT DOMAIN 109 118

FT DOMAIN 119 129

FT DOMAIN 119 129

FT DISULFID 43 108

FT NON\_TER 129 129

SQ SEQUENCE 129 AA; 14375 MW; 2F344968 CRC32;

Query Match 83.6%; Score 637; DB 5; Length 129;

Best Local Similarity 83.0%; Pred No. 2.45e-119;

Matches 88; Conservative 12; Mismatches 4; Indels 2; Gaps 2;

Db 24 ltsqptslsppgeratlsralscrasqsvsnflawyqkpgqgprlllyvassratgipdrf 82

QY 3 LTQSPGTLISLSPGERATLSRALSQSVSSNYLAWYQKPGQGPRLLYVASSRATGIPDRF 82

Db 83 ssgsgtdftltisrlepedfavyycqygsspsstfaggtkveik 128

QY 63 SSGSGTDFTLTISRLEPEDFAVYCYQLYGNRMTFGGTKEIK 107

RESULT 9

ID KV3C\_HUMAN STANDARD: PRT: 100 AA

AC P01621;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN PRECURSOR V-III REGION (R6) (RHEUMATOID FACTOR).

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 84093600.

RA BENTLEY D.L.;

PL NATURE 307:77-80(1984).

CC -1- THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.

DR PIR: A01894; K3HUG1.

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DR HSSP: P01607: 1AAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL: HYBRIDOMA.
FT NON_TER 1 1 4
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NGS).
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 99A75223 CRC32;

Query Match 81.6%; Score 622; DB 5; Length 100;
Best Local Similarity 93.5%; Pred. No. 7.55e-115;
Matches 87; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 8 ltqspgtlslspgeratlscrasqsvssylawyqkqgqprlllygatsratgipdrf 67
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSPATGIPDPF 62

Db 68 sgsasgtdftltisrlepedfavyvccqyansq 100
QY 63 SSGSGGTDFTLTISRLEPEDFAVYVCCYQYGNR 95

RESULT 10
ID KV3K_HUMAN STANDARD: PPT: 128 AA
AC P06311;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041852.
RA KLOBECK H.G., MEINDL A., COMERIATO G., SOLOMON A., ZACHAU H.G.:
RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR EMBL; Z00021; G33179; -.
DR PIR; A01899; K3HU41.
DR HSSP: P01607: 3HFM.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 80.2%; Score 611; DB 5; Length 128;
Best Local Similarity 85.7%; Pred. No. 2.71e-112;
Matches 90; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Db 24 ltqspgtlslspgeratlscrasqsvsn-lawyqkqgqprlllydassrangipdrf 82
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSPATGIPDPF 62

Db 83 sgsasgtdftltisrlepedfavyvccqyatspytggqtkleik 127
QY 63 SSGSGGTDFTLTISRLEPEDFAVYVCCYQYGNRWTGQGTKEIK 107

RESULT 11
ID KV3F_HUMAN STANDARD: PPT: 109 AA.
AC P01624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
PN [1]
RP SEQUENCE.
PA KLAPPER D.G., CAPP A J.D.;
PL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976)
CC -I- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR; A01897; K3HUPM.
DR HSSP: P01607; 1DEB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; A0C42C88 CRC32;

Query Match 79.4%; Score 605; DB 5; Length 109;
Best Local Similarity 79.0%; Pred. No. 6.69e-111;
Matches 83; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Db 4 mtqspvtlsvpgeratlscrasqslscslylawyqkqpsqsprrlllygastatgiparf 63
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSPATGIPDPF 62

Db 64 sgsasgtdftltisrlepedfavyvccqyannwppfagatveik 108
QY 63 SSGSGGTDFTLTISRLEPEDFAVYVCCYQYGNRSPWTFGQGTKEIK 107

RESULT 12
ID KV3I_HUMAN STANDARD: PPT: 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85087932.
PA PECH M., ZACHAU H.G.;
PL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL; X01668; ; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E18JFC CRC32;

Query Match 73.5%; Score 560; DB 5; Length 115;
Best Local Similarity 92.0%; Pred. No. 1.72e-100;
Matches 80; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Db 24 ltqspgtlslspgeratlscrasqsvss-lawyqkqgqprlllydasnatgiparf 82
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSPATGIPDPF 62

Db 83 sgsasgtdftltisrlepedfavyvccq 109
QY 63 SSGSGGTDFTLTISRLEPEDFAVYVCCQ 89

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RESULT 13  
 ID KV3J.HUMAN STANDARD: PRT: 116 AA.  
 AC P04434:  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT)  
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT)  
 OS HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 85087332.  
 RA PECH M., ZACHAU H.G.  
 PC NUCLEIC ACIDS RES 12:9229-9236(1984)  
 DR EMRL: X02725; :; NOT\_ANNOTATED\_IDS.  
 DR PIR: A01901; K3HUVH.  
 DR HSSP: P01607; IMCP.  
 KW IMMUNOGLOBULIN V REGION: SIGNAL.  
 FT SIGNAL 1 20  
 FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH)  
 FT DOMAIN 21 43 FRAMEWORK 1  
 FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1  
 FT DOMAIN 44 55 FRAMEWORK 2  
 FT DOMAIN 56 70 FRAMEWORK 3  
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2  
 FT DOMAIN 78 109 FRAMEWORK 3  
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3  
 FT DISULFID 43 109 BY SIMILARITY.  
 FT NON-TER 116  
 SQ SEQUENCE 116 AA: 12757 MW: 27FA1BCE CPO32:  
 Query Match 73.2%: Score 558; DB 5; Length 116;  
 Best Local Similarity 87.4%: Pred. No. 4 99e-100;  
 Matches 76; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 Db 24 mtgspstlsppervlscrasqssvssyltwyqkpgaprllygastatrsiparf 83  
 QY 3 LTQSPGTLSPGERATLSGASQSSVSSNYLAWYQPPGQAPPLLYGASSPATGIPDRF 62  
 Db 84 sgsqsgtdftltisslqpedfavyvqc 110  
 QY 63 SGSGSGTDFTLTISRLEPEDFAVYVQC 89  
 RESULT 14  
 ID KVM.HUMAN STANDARD: PRT: 108 AA  
 AC P01605:  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (LAV).  
 DE IG KAPPA CHAIN V-I REGION (LAV).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE: 7703198  
 RA CAPRA J.D., KLAPPER D.G.  
 HL SCAND. J. IMMUNOL. 5:675-684(1976).  
 CC -1- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN PM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.  
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.  
 DR PIR: A01871; K1HJLY.  
 DR HSSP: P01607; 2FGW.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 FRAMEWORK 3.  
 FT DOMAIN 57 98 FRAMEWORK 4.  
 FT DISULFID 23 98 BY SIMILARITY.  
 FT NON-TER 108  
 SQ SEQUENCE 108 AA: 11840 MW: 88AD251 CPO32:  
 Query Match 60.4%: Score 529; DB 5; Length 108;  
 Best Local Similarity 53.2%: Pred. No. 4 01e-93;  
 Matches 67; Conservative 23; Mismatches 15; Indels 1; Gaps 1;  
 Db 3 qmtqpsissasvqdrvtltorasqdrindltwyqkpgatpkrlyyatslqsyvpsr 61  
 QY 2 ELTQSPGTLSPGERATLSGASQSSVSSNYLAWYQPPGQAPPLLYGASSPATGIPDR 61  
 Db 62 fsgsgsgtdftltisslqpedfavyvqc 107  
 QY 62 FSQSGSGTDFTLTISRLEPEDFAVYVQSGTGGTKEIK 107

Search completed: Tue Feb 24 07:17:24 1998  
 Job time : 14 secs.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON-TER 108  
 SQ SEQUENCE 108 AA: 11934 MW: 22228PQC CPO32:  
 Query Match 70.5%: Score 537; DB 5; Length 108;  
 Best Local Similarity 67.0%: Pred. No. 3 42e-95;  
 Matches 71; Conservative 21; Mismatches 13; Indels 1; Gaps 1;  
 Db 3 qmtqpsissasvqdrvtltorasqdrindltwyqkpgatpkrlyyatslqsyvpsr 61  
 QY 2 ELTQSPGTLSPGERATLSGASQSSVSSNYLAWYQPPGQAPPLLYGASSPATGIPDR 61  
 Db 62 fsgsgsgtdftltisslqpedfavyvqc 107  
 QY 62 FSQSGSGTDFTLTISRLEPEDFAVYVQSGTGGTKEIK 107  
 RESULT 15  
 ID KVM.HUMAN STANDARD: PRT: 108 AA.  
 AC P01610:  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (WEA).  
 DE IG KAPPA CHAIN V-I REGION (WEA).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE: 83273707.  
 RA GONI F., FRANGIONE B.;  
 PL PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).  
 CC -1- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST WALDENSTROM'S MACROGLOBULINEMIA.  
 CC 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH PIR, A01876; K1HWE.  
 DR HSSP: P01607; 2FGW.  
 KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON-TER 108  
 SQ SEQUENCE 108 AA: 11840 MW: 88AD251 CPO32:  
 Query Match 60.4%: Score 529; DB 5; Length 108;  
 Best Local Similarity 53.2%: Pred. No. 4 01e-93;  
 Matches 67; Conservative 23; Mismatches 15; Indels 1; Gaps 1;  
 Db 3 qmtqpsissasvqdrvtltorasqdrindltwyqkpgatpkrlyyatslqsyvpsr 61  
 QY 2 ELTQSPGTLSPGERATLSGASQSSVSSNYLAWYQPPGQAPPLLYGASSPATGIPDR 61  
 Db 62 fsgsgsgtdftltisslqpedfavyvqc 107  
 QY 62 FSQSGSGTDFTLTISRLEPEDFAVYVQSGTGGTKEIK 107





**authors** Kipps, T. J.; Tomhave, E.; Chen, P. P.; Carson, D.A.  
**journal** J. Exp. Med. (1988) 167:840-852  
**title** Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.  
**cross-references** MUID:88171307  
**accession** P00021  
**molecule\_type** mRNA  
**residues** 1-129 #label KIP  
**comment** The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
**GENETICS**  
**gene** GDB:IGKV3  
**cross-references** GDB:136266  
**complex**  
 An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
**CLASSIFICATION**  
**keywords** superfamily immunoglobulin V region; immunoglobulin homology autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin  
**FEATURE**  
 1-20 #domain signal sequence #status predicted #label SIG  
 21-129 #product Ig kappa chain V-III region (Hic) #status predicted #label MAR  
 21-117 #region V segment  
 44-55 #region complementarity-determining 1\  
 71-77 #region complementarity-determining 2\  
 110-117 #region complementarity-determining 3\  
 118-129 #region J segment (JK1)  
 43-109 #disulfide\_bonds #status predicted  
**SUMMARY**  
 #length 129 #molecular\_weight 14070 #checksum 8174  
 Query Match 93.4%; Score 712; DB 2; Length 129;  
 Best Local Similarity 94.3%; Pred. No. 2.17e-63;  
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Db 24 ltsgpgtltlspggratlsgrasqvssylawyqkqpgqprlliygassratgipdrf 83  
 Qy 3 LTQSPGTLSPGGRATLSGRASQVSSSNLYAWYQRPQAPRLIYGCASSPATGIPDRF 62  
 Db 84 sgsgsgtdftltisrlepedfavyycqygspwtfgggtkveik 128  
 Qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSWTFGGGTKEIK 107  
**RESULT** 3  
**ENTRY**  
**TITLE** Ig kappa chain V region (G6+ CLL-BRA) - human (fragment)  
**ORGANISM** #formal\_name Homo sapiens #common\_name man  
**DATE** 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
**ACCESSIONS** PH0965  
**REFERENCE** PH0952  
**authors** Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
**journal** J. Exp. Med. (1992) 175:983-991  
**title** Evidence for somatic selection of natural autoantibodies.  
**cross-references** MUID:92202880  
**accession** PH0965  
**status** nucleic acid sequence not shown  
**molecule\_type** DNA  
**residues** 1-107 #label MAR  
**CLASSIFICATION** superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin  
**KEYWORDS**  
**FEATURE**  
 1-21 #region framework 1\  
 22-32 #region complementarity-determining 1\  
 33-48 #region framework 2\  
 49-54 #region complementarity-determining 2\  
 55-87 #region framework 3\

**88-95** #region complementarity-determining 3  
**SUMMARY** #length 107 #checksum 7830  
 Query Match 93.2%; Score 710; DB 7; Length 107;  
 Best Local Similarity 95.2%; Pred. No. 3.63e-63;  
 Matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Db 2 ltsgptltlspggratlsgrasqvssylawyqkqpgqprlliygassratgipdrf 61  
 Qy 3 LTQSPGTLSPGGRATLSGRASQVSSSNLYAWYQRPQAPRLIYGCASSPATGIPDRF 62  
 Db 62 sgsgsgtdftltisrlepedfavyycqygspwtfgggtkveik 106  
 Qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSWTFGGGTKEIK 107  
**RESULT** 4  
**ENTRY**  
**TITLE** D30601 #type fragment  
**ORGANISM** Ig kappa chain V-III region (Cur) - human (fragment)  
**DATE** #formal\_name Homo sapiens #common\_name man  
 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
**ACCESSIONS** D30601  
**REFERENCE** A30601  
**authors** Goni, F.; Chen, P. P.; McGinnis, D.; Arjonilla, M. L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.  
**journal** J. Immunol. (1989) 142:3158-3163  
**title** Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.  
**cross-references** MUID:89215279  
**accession** D30601  
**status** preliminary  
**molecule\_type** protein  
**residues** 1-109 #label GON  
**CLASSIFICATION** superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin  
**KEYWORDS**  
**SUMMARY** #length 109 #checksum 6151  
 Query Match 92.1%; Score 702; DB 7; Length 109;  
 Best Local Similarity 94.3%; Pred. No. 2.85e-62;  
 Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Db 4 ltsgptltlspggratlsgrasqvssylawyqkqpgqprlliygassratgipdrf 63  
 Qy 3 LTQSPGTLSPGGRATLSGRASQVSSSNLYAWYQRPQAPRLIYGCASSPATGIPDRF 62  
 Db 64 sgsgsgtdftltisrlepedfavyycqygspwtfgggtkveik 108  
 Qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSWTFGGGTKEIK 107  
**RESULT** 5  
**ENTRY**  
**TITLE** K3HUA #type complete  
**ORGANISM** Ig kappa chain precursor V-III region (Hah) - human  
**DATE** #formal\_name Homo sapiens #common\_name man  
 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 30-May-1997  
**ACCESSIONS** P10022  
**REFERENCE** P10021  
**authors** Kipps, T.J.; Tomhave, E.; Chen, P.F.; Carson, D.A.  
**journal** J. Exp. Med. (1988) 167:840-852  
**title** Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.  
**cross-references** MUID:88171307  
**accession** P10022  
**molecule\_type** mRNA  
**residues** 1-129 #label KIP  
**COMMENT** The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
**GENETICS**

```

#gene
#cross-references GDB:136266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS autoantibody; chronic lymphocytic leukemia; heterotetramer;
immunoglobulin
FEATURE
1-20 *domain signal sequence #status predicted #label SIG
21-129 *product Ig kappa chain V-III region (Hah) #status
predicted #label MAT
21-117 *region V segment
44-55 *region complementarity-determining 1\
71-77 *region complementarity-determining 2\
110-117 *region complementarity-determining 3\
118-124 *region J segment (Jk1)\
43-109 *disulfide_bonds #status predicted
SUMMARY *length 129 #molecular-weight 14073 #checksum 7361
Query Match 92.9% Score 701 DB 2 Length 129
Best Local Similarity 94.3% Pred No 3 68e-62
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltspgtlspgeratlscrasqsvssylawyqkpgqaprllygassratgipdrf 83
QY 3 LTQSPGTLSPGERATLSRLEPEDFAVYCYQLYGNRPWFQGGTKVEIK 107

Db 84 sqsgsgtdftltisrlepedfavyycqygssplrtfgqgatkveik 128
QY 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRPWFQGGTKVEIK 107

RESULT 6
ENTRY B30601 #type fragment
TITLE Ig kappa chain V-III region (Pay) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS C30601
REFERENCE A30601
#authors Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references M31D:89215279
#accession C30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5191
Query Match 91.9% Score 700 DB 7 Length 109
Best Local Similarity 95.2% Pred No 4 75e-62
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltspgtlspgeratlscrasqsvssylawyqkpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSRLEPEDFAVYCYQLYGNRPWFQGGTKVEIK 107

Db 64 sqsgsgtdftltisrlepedfavyycqygssplrtfgqgatkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRPWFQGGTKVEIK 107

RESULT 7
ENTRY B30601 #type fragment
TITLE Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
15-Aug-1996

```

```

ACCESSIONS H30601; E30601
REFERENCE A30601
#authors Gonl, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
          Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
          Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotype characterization of the L chains of
#cross-references MUID:89215279
#accession H30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON1
#accession E30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON2
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5951

Query Match 91.1%; Score 694; DB 7; Length 109;
Best Local Similarity 93.3%; Pred. No. 2.23e-61;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltsgptslspgeratlsqrasqsvssylawygkqkqaprllyqasratgipdrf 63
QY 3 LTOSPTLSLSPGERATLSQPASQSVSSNYLAWYQQRCPAPRLLYGASSRATGIPDRF 62

Db 64 sgsgsgtdftltisrlepedfavyycqygsspytfqggtkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 10
ENTRY F44151 #type fragment
TITLE Ig kappa chain V region (JM-01) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS F44151
REFERENCE A44151
#authors Zebadee, S.L.; Barbas III, C.F.; Hwu, Y.L.; Caotih-n, F.H.;
          Graff, R.; DeGraw, J.; Pyati, J.; LaPolla, R.; Burton,
          D.P.; Lerner, P.A.; Thornton, G.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface
          antigen.
#accession F44151
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-109 ##label ZEB
##note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5518

Query Match 90.8%; Score 692; DB 7; Length 109;
Best Local Similarity 91.6%; Pred. No. 3.73e-61;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 aeltspgtslspgeratlsqrasqsvfnylawygkqkqaprllyqasratgipdrf 60
QY 1 AELTSPGTLSLSPGERATLSQRASQSVSSNYLAWYQQRCPAPRLLYGASSRATGIPDRF 60

Db 61 rfsgsgsgtdftltisrlepedfavyycqygsspytfqggtkveik 107
QY 61 RFSGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 11
ENTRY F30607 #type fragment
TITLE Ig kappa chain V-III region (Bor) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man

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```

ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS F30607
REFERENCE A30601
#authors Gonl, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
          Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
          Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotype characterization of the L chains of
#cross-references MUID:89215279
#accession F30607
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6514

Query Match 90.8%; Score 692; DB 7; Length 109;
Best Local Similarity 94.3%; Pred. No. 3.73e-61;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltsgptslspgeratlsqrasqsvssylawygkqkqaprllyqasratgipdrf 63
QY 3 LTOSPTLSLSPGERATLSQRASQSVSSNYLAWYQQRCPAPRLLYGASSRATGIPDRF 62

Db 64 sgsgsgtdftltisrlepedfavyycqygsspytfqggtkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 12
ENTRY G30601 #type fragment
TITLE Ig kappa chain V-III region (Got) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS G30601
REFERENCE A30601
#authors Gonl, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
          Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
          Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotype characterization of the L chains of
#cross-references MUID:89215279
#accession G30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5641

Query Match 90.7%; Score 691; DB 7; Length 109;
Best Local Similarity 92.4%; Pred. No. 4.82e-61;
Matches 97; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltsgptslspgeratlsqrasqsvrnylawygkqkqaprllyqasratgipdrf 63
QY 3 LTOSPTLSLSPGERATLSQPASQSVSSNYLAWYQQRCPAPRLLYGASSRATGIPDRF 62

Db 64 sgsgsgtdftltisrlepedfavyycqygsspytfqggtkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 13
ENTRY S20635 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man

```

```

DATE          20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
              16-Aug-1996
ACCESSIONS    S20635
REFERENCE      S20631
#authors      Lee, S. K. ; Bridges, L. S. ; Koopman, W. T. ; Schroeder, H. W.
#submissions  submitted to the EMBL Data Library, April 1992
#accession    S20635
#status       preliminary
#molecule_type mRNA
#residues     1-110 #label LEE
#cross-references EMBL:211893
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 110 #molecular-weight 11965 #checksum 136

Query Match   90.4%; Score 689; DB 7; Length 110;
Best Local Similarity 91.4%; Pred. No. 8.07e-61;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 6 ltspqtlslpgeratiscrasgsvtynylgwygkpgqaprllygassratgipdrf 65
    |||||
Qy 3 LTQSPGTLSPGGERATLSCPASQSVSSNVLAWYQQPQPGAPRLLYGASSPATGIPDRF 62
    |||||

Db 66 sgsqsgtdftltisrlepedfavyycqyqdsprtfqggtkveik 110
    |||||
Qy 63 SGSGSGTDFTLTISRLEPEFAVYCYQLYGNRWTFGQGTKEIK 107
    |||||

RESULT 14
ENTRY      PH0963 #type fragment
TITLE      Ig kappa chain V region (G6+ CLL-SM1) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
              16-Aug-1996
ACCESSIONS PH0963
REFERENCE    PH0952
#authors     Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal     J. Exp. Med. (1992) 175:983-991
#title       Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession   PH0963
#status      nucleic acid sequence not shown
#molecule_type DNA
#residues    1-109 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       1-23 #region framework 1\
              24-34 #region complementarity-determining 1\
              35-50 #region framework 2\
              51-56 #region complementarity-determining 2\
              57-89 #region framework 3\
              90-97 #region complementarity-determining 3
              #length 109 #checksum 5292
SUMMARY

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Best Local Similarity 93.3%; Pred. No. 1.04e-60;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy 3 LTQSPGTLSPGGERATLSCPASQSVSSNVLAWYQQPQPGAPRLLYGASSPATGIPDRF 62
    |||||

Db 64 sgsqsgtdftltisrlepedfavyycqyqssppafaggtkveik 108
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Qy 63 SGSGSGTDFTLTISRLEPEFAVYCYQLYGNRWTFGQGTKEIK 107
    |||||

RESULT 15
ENTRY      A30608 #type fragment
TITLE      Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change

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              16-Aug-1996
ACCESSIONS    A30608
REFERENCE      A30601
#authors      Gotti, F.R.; Chen, F.P.; McGinnis, D.; Arjonilla, M.L.;
              Fernandez, J.; Carson, D.; Solomon, A.; Mender, E.;
              Frangione, B.
#journal       J. Immunol. (1989) 142:3158-3163
#title         Structural and idiotypic characterization of the L chains of
              human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession     A30608
#status        preliminary
#molecule_type protein
#residues      1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 6031

Query Match   90.2%; Score 687; DB 7; Length 109;
Best Local Similarity 92.4%; Pred. No. 1.35e-60;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltspqtlslpgeratiscrasgsvssylawygkpgqaprllygassratgipdrf 63
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Db 64 sgsqsgtdftltisrlepedfavyycqyqsspytfaggtkveik 108
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Qy 63 SGSGSGTDFTLTISRLEPEFAVYCYQLYGNRWTFGQGTKEIK 107
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Search completed: Tue Feb 24 07:18:03 1998
Job time : 21 secs.

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RESULT 2
ID US-08-276-852-86 STANDARD: PRT: 108 AA.
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AC xxxxxx
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DT 01-JAN-1900
XX
DE Sequence 86, Application US/08276852.
XX
CC Sequence 86, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCP1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65957 CN;

Query Match 91.5%; Score 697; DB 7; Length 108;
Best Local Similarity 92.5%; Pred No 1 95e-46; Indels 0; Gaps 0;
Matches 98; Conservative 2; Mismatches 6;

Db 1 ELTQSPGTLSPGERATLSRQASQVSNLYAWYQKPGCAPPLLIYGVSNRATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSRQASQVSNLYAWYQKPGCAPPLLIYGVSNRATGIPDR 61
Db 61 FSGSGSGDTFLTISRLEPEFAVYCYQHYGNSVITFGQTKLEIK 106
QY 62 FSGSGSGDTFLTISRLEPEFAVYCYQHYGNSVITFGQTKLEIK 107

RESULT 3
ID PCT-US95-08743-90 STANDARD: PRT: 107 AA
XX
AC xxxxxx
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DT 01-JAN-1900
XX
DE Sequence 90, Application US/08276852.
XX
CC Sequence 90, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCP1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65957 CN;

Query Match 91.5%; Score 697; DB 7; Length 108;
Best Local Similarity 92.5%; Pred No 1 95e-46; Indels 0; Gaps 0;
Matches 98; Conservative 2; Mismatches 6;

Db 1 ELTQSPGTLSPGERATLSRQASQVSNLYAWYQKPGCAPPLLIYGVSNRATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSRQASQVSNLYAWYQKPGCAPPLLIYGVSNRATGIPDR 61
Db 61 FSGSGSGDTFLTISRLEPEFAVYCYQHYGNSVITFGQTKLEIK 106
QY 62 FSGSGSGDTFLTISRLEPEFAVYCYQHYGNSVITFGQTKLEIK 107

RESULT 4
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AC xxxxxx
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DT 01-JAN-1900
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DE Sequence 90, Application US/08276852.
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CC Sequence 90, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCP1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
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CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11705 MW; 62938 CN;

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Best Local Similarity 89.8%; Pred No 1 80e-45;
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Db 1 ELTQSPGTLSPGERATLSRQASQVSNLYAWYQKPGCAPPLLIYGVSNRATGIPDR 60
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Db 61 FSGSGSGDTFLTISRLEPEFAVYCYQHYGNSVITFGQTKLEIK 106
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DT 01-JAN-1900
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DE Sequence 90, Application PC/TUS9508743.
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CC Sequence 90, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 90:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
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Db 1 ELTQSPGTLSPGERATLSRQASQVSNLYAWYQKPGCAPPLLIYGVSNRATGIPDR 60
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AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 90, Application US/08276852.
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CC Sequence 90, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
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CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/276,852  
 CC FILING DATE: 18-JUL-1994  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SCRI452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 90:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 107 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
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 CC SEQUENCE 107 AA: 11705 MW: 52938 CN:

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 Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

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RESULT 5  
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 XX xxxxxx  
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 XX 01-JAN-1900  
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 XX Sequence 86, Application US/08477728.

XX Sequence 86, Application US/08477728  
 CC Patent No. 5585089  
 CC GENERAL INFORMATION:  
 CC APPLICANT: QUEEN, Cary L.  
 CC APPLICANT: SCHNEIDER, William P.  
 CC APPLICANT: SELICK, Harold E.  
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 CC NUMBER OF SEQUENCES: 113  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Townsend and Crew LLP  
 CC STREET: Two Embarcadero Center, 8th Floor  
 CC CITY: Palo Alto  
 CC STATE: California  
 CC COUNTRY: US  
 CC ZIP: 94111  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/477,728

CC FILING DATE: 07-JUN-1995  
 CC CLASSIFICATION: 424  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/634,278  
 CC FILING DATE: 19-DEC-1990  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/590,274  
 CC FILING DATE: 28-SEP-1990  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/310,252  
 CC FILING DATE: 13-FEB-1989  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/290,975  
 CC FILING DATE: 28-DEC-1988  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Smith, William M  
 CC REGISTRATION NUMBER: 30,223  
 CC REFERENCE/DOCKET NUMBER: 11823-002600  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 326-2400  
 CC TELEFAX: (415) 326-2422  
 CC INFORMATION FOR SEQ ID NO: 86:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 108 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: peptide  
 CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 89.9%; Score 685; DB 6; Length 108;  
 Best Local Similarity 92.4%; Pred. No. 1.80e-45;  
 Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 LTQSPGTLSPGERATLSPASQSVSSNNYLAWYQKPGQAPPLLYGSSRATGIPDR 63  
 QY 3 LTQSPGTLSPGERATLSPASQSVSSNNYLAWYQKPGQAPPLLYGSSRATGIPDR 62  
 Db 64 SSGSGSGDTFTLISRLPEDFAVYCOHYGNSVTFQGGTKLEIK 108  
 QY 63 SSGSGSGDTFTLISRLPEDFAVYCOHYGNSVTFQGGTKLEIK 107

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 ID US-08-474-040-86 STANDARD: PRT: 108 AA.  
 XX xxxxxx  
 AC  
 XX 01-JAN-1900  
 DT  
 XX Sequence 86, Application US/08474040.

XX Sequence 86, Application US/08474040  
 CC Patent No. 5693761  
 CC GENERAL INFORMATION:  
 CC APPLICANT: QUEEN, Cary L.  
 CC APPLICANT: CO. Man Sung  
 CC APPLICANT: SCHNEIDER, William P.  
 CC APPLICANT: LANDOLFI, Nicholas F.  
 CC APPLICANT: COELINGH, Kathleen L.  
 CC APPLICANT: SELICK, Harold E.  
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 CC NUMBER OF SEQUENCES: 113  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew  
 CC STREET: 379 Lytton Avenue  
 CC CITY: Palo Alto  
 CC STATE: California  
 CC COUNTRY: US  
 CC ZIP: 94301  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/474,040  
 CC FILING DATE: 07-JUN-1995  
 CC CLASSIFICATION: 536  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/634,278  
 CC FILING DATE: 19-DEC-1990  
 CC APPLICATION NUMBER: US 07/590,274  
 CC FILING DATE: 28-SEP-1990  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/310,252  
 CC FILING DATE: 13-FEB-1989  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/290,975  
 CC FILING DATE: 28-DEC-1988  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Smith, William M.  
 CC REGISTRATION NUMBER: 30,223  
 CC REFERENCE/DOCKET NUMBER: 11823-002600  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 326-2400  
 CC TELEFAX: (415) 326-2422  
 CC INFORMATION FOR SEQ ID NO: 86:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 108 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: peptide  
 CC SEQUENCE 108 AA: 11590 MW: 64079 CN;  
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 CC Query Match 89.9%; Score 685; DB 7; Length 108;  
 CC Best Local Similarity 92.4%; Pred No 1.80e-45;  
 CC Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
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 QY 3 LTQSPGTLSPGERATLSCPASQSVSSNLAWYQQPQPGAPRLIYGCASSRATGIPDPF 62  
 Db 64 SGSGSGTDFTLTISRLEPEDFAVYQCQYSGISGRTFGQGTKEIK 108  
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 RESULT 7  
 ID US-07-634-278-86 STANDARD: PPT: 108 AA  
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 AC xxxxxx  
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 DT 01-JAN-1900  
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 DE Sequence 86, Application US/07634278.  
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 CC Sequence 86, Application US/07634278  
 CC Patent No. 5530101  
 CC GENERAL INFORMATION:  
 CC APPLICANT: QUEEN, Cary L.  
 CC APPLICANT: CO, Man Sung  
 CC APPLICANT: SCHNEIDER, William P.  
 CC APPLICANT: LANDOLFI, Nicholas F.  
 CC APPLICANT: COELINGH, Kathleen L.  
 CC APPLICANT: SELICK, Harold E.  
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 CC NUMBER OF SEQUENCES: 113  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew  
 CC STREET: 379 Lytton Avenue  
 CC CITY: Palo Alto  
 CC STATE: California  
 CC COUNTRY: US  
 CC ZIP: 94301

CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/07/634,278  
 CC FILING DATE: 19-DEC-1990  
 CC CLASSIFICATION: 424  
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 CC APPLICATION NUMBER: US 07/590,274  
 CC FILING DATE: 28-SEP-1990  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/310,252  
 CC FILING DATE: 13-FEB-1989  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/290,975  
 CC FILING DATE: 28-DEC-1988  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Smith, William M.  
 CC REGISTRATION NUMBER: 30,223  
 CC REFERENCE/DOCKET NUMBER: 11823-002600  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 326-2400  
 CC TELEFAX: (415) 326-2422  
 CC INFORMATION FOR SEQ ID NO: 86:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 108 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: peptide  
 CC SEQUENCE 108 AA: 11590 MW: 64079 CN;  
 CC  
 CC Query Match 89.9%; Score 685; DB 6; Length 108;  
 CC Best Local Similarity 92.4%; Pred. No. 1.80e-45;  
 CC Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
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 Db 4 LTQSPGTLSPGERATLSCPASQSVSSGVLGWYQKPGQAPRLIYGCASSRATGIPDPF 63  
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 ID US-08-487-200-86 STANDARD: PPT: 108 AA  
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 AC xxxxxx  
 XX  
 DT 01-JAN-1900  
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 DE Sequence 86, Application US/08487200.  
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 CC Sequence 86, Application US/08487200  
 CC Patent No. 5693762  
 CC GENERAL INFORMATION:  
 CC APPLICANT: QUEEN, Cary L.  
 CC APPLICANT: CO, Man Sung  
 CC APPLICANT: SCHNEIDER, William P.  
 CC APPLICANT: LANDOLFI, Nicholas F.  
 CC APPLICANT: COELINGH, Kathleen L.  
 CC APPLICANT: SELICK, Harold E.  
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 CC NUMBER OF SEQUENCES: 113  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Townsend and Crew  
 CC STREET: 379 Lytton Avenue  
 CC CITY: Palo Alto  
 CC STATE: California  
 CC COUNTRY: US

CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/487,200  
CC FILING DATE: 7-JUN-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/634,278  
CC FILING DATE: 19-DEC-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/590,274  
CC FILING DATE: 28-SEP-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/310,252  
CC FILING DATE: 13-FER-1989  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/290,975  
CC FILING DATE: 28-DEC-1988  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Smith, William M  
CC REGISTRATION NUMBER: 30,223  
CC REFERENCE/DOCKET NUMBER: 11823-002610  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 326-2400  
CC TELEFAX: (415) 326-2422  
CC INFORMATION FOR SEQ ID NO: 86:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:  
Query Match 89.9%; Score 685; DB 7; Length 108;  
Best Local Similarity 92.4%; Pred. No. 1.80e-45;  
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 LTQSPGTLSPGERATLSCPASQSVSSNYLAWYQCPQAPPLIYGCSSPATGIPDRF 63  
QY 3 LTQSPGTLSPGERATLSCPASQSVSSNYLAWYQCPQAPPLIYGCSSPATGIPDRF 62  
Db 64 SGGSGGTDFTLTISRLEPEDFAVYQCQYGLGRTFGGKVEIK 108  
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ID PCT-US95-08743-99 STANDARD; PRT: 108 AA.  
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AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 99, Application PC/TUS9508743.  
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CC Sequence 99, Application PC/TUS9508743  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC COMPUTER READABLE FORM: disk  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (FPO)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/08743

CC FILING DATE: 11-JUL-1995  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/276,852  
CC FILING DATE: 18-JUL-1994  
CC INFORMATION FOR SEQ ID NO: 99:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 108 AA: 11738 MW: 63142 CN:  
Query Match 89.8%; Score 684; DB 13; Length 108;  
Best Local Similarity 88.7%; Pred. No. 2.17e-45;  
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSCRAQGSISSNLYAWYQKQCPQAPPLIYGCSSPATGIPDR 60  
QY 2 ELTQSPGTLSPGERATLSCRAQGSISSNLYAWYQKQCPQAPPLIYGCSSPATGIPDR 61  
Db 61 FSGSGGTDFTLTISRLEPEDFAVYQCQYGTSPYTFGGTQIDIK 106  
QY 62 FSGSGGTDFTLTISRLEPEDFAVYQCQYGLGNSRWTFGGKVEIK 107

RESULT 10  
ID US-08-276-852-99 STANDARD; PRT: 108 AA.  
XX  
XX AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 99, Application US/08276852.  
CC  
CC Sequence 99, Application US/08276852  
CC Patent No. 5652138  
CC GENERAL INFORMATION:  
CC APPLICANT: Burton, Dennis R  
CC APPLICANT: Barbas, Carlos F  
CC APPLICANT: Lerner, Richard A  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: The Scripps Research Institute, Office of  
CC ADDRESSEE: Patent Counsel  
CC STREET: 10666 No 5652138th Torrey Pines Road, Suite 220,  
CC STREET: Mail Drop IPC8  
CC CITY: La Jolla  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/276,852  
CC FILING DATE: 18-JUL-1994  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/178,302  
CC FILING DATE: 30-SEP-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/954,148  
CC FILING DATE: 30-SEP-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: SCRI452P  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312  
CC INFORMATION FOR SEQ ID NO: 99:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 108 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 108 AA; 11738 MW; 63142 CN;  
  
Query Match 89.8%; Score 684; DB 7; Length 108;  
Best Local Similarity 88.7%; Pred. No. 2.17e-45;  
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
  
Db 1 ELTQSPGTLSPGERATLSRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 106  
QY 2 ELTQSPGTLSPGERATLSRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 107  
  
Db 61 FSGSGSGTDTLTISRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 106  
QY 62 FSGSGSGTDTLTISRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 107  
  
RESULT 11  
ID PCT-US93-08786-23 STANDARD: PPT: 109 AA  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 23, Application PC/TUS9308786.  
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CC Sequence 23, Application PC/TUS9308786  
CC GENERAL INFORMATION:  
CC APPLICANT: Burton, Dennis R.  
CC APPLICANT: Barbas, III, Carlos F.  
CC APPLICANT: Chanock, Robert M.  
CC APPLICANT: Murphy, Brian R.  
CC APPLICANT: Crowe, Jr., James E.  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS  
CC NUMBER OF SEQUENCES: 29  
CC CORRESPONDENCE ADDRESS:  
CC STREET: Spensley Horn Jubas & Lubitz  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/08786  
CC FILING DATE: 16-SEP-1993  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Wetherell, Jr., Ph.D., John R.  
CC REGISTRATION NUMBER: 31,678  
CC REFERENCE/DOCKET NUMBER: FD-2791  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 455-5100  
CC TELEFAX: (619) 455-5110  
CC INFORMATION FOR SEQ ID NO: 23:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 109 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC IMMEDIATE SOURCE:  
CC CLONE: rsv 6L 11L 21L; anad 22L

CC FEATURE:  
CC NAME/KEY: Peptide  
CC LOCATION: 1..109  
CC SEQUENCE 109 AA; 12099 MW; 62556 CN;  
  
Query Match 89.6%; Score 683; DB 11; Length 109;  
Best Local Similarity 89.7%; Pred. No. 2.61e-45;  
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
  
Db 2 AELTQSPGTLSPGERATLSRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 108  
QY 1 AELTQSPGTLSPGERATLSRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 109  
  
Db 62 FSGSGSGTDTLTISRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 108  
QY 61 FSGSGSGTDTLTISRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 107  
  
RESULT 12  
ID PCT-US95-08743-147 STANDARD: PPT: 109 AA  
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AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 147, Application PC/TUS9508743.  
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CC Sequence 147, Application PC/TUS9508743  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC NUMBER OF SEQUENCES: 170  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPC)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/08743  
CC FILING DATE: 11-JUL-1995  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/276,852  
CC FILING DATE: 18-JUL-1994  
CC INFORMATION FOR SEQ ID NO: 147:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 109 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 109 AA; 11779 MW; 65550 CN;  
  
Query Match 89.2%; Score 680; DB 13; Length 109;  
Best Local Similarity 91.6%; Pred. No. 4.55e-45;  
Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;  
  
Db 2 AELTQSPGTLSPGERATLSRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 108  
QY 1 AELTQSPGTLSPGERATLSRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 109  
  
Db 62 FSGSGSGTDTLTISRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 107  
QY 61 FSGSGSGTDTLTISRLEPEDFAVYCOQYGTSPVTFGGTGOLDIK 107  
  
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XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 147, Application US/08276852

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XX
CC Sequence 147, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10656 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 147:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA; 11779 MW; 65550 CN;
CC
CC Query Match 89.2%; Score 680; DB 7; Length 109;
CC Best Local Similarity 91.6%; Pred. No. 4.55e-45;
CC Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps
CC
Db
2 AELTQSPGTLSPGERAVIVSCRASQSVSNVLAWYQKPGQAPRLIYGASNRATGIPD
QY 1 AELTQSPGTLSPGERATISCRASQSVSNVLAWYQKPGQAPRLIYGASNRATGIPD
Db
62 RFGSGSGGTDTLTISRLEPEDFAVYYCQYQSSG-TFGQGTKEIK 107
QY 61 RFGSGSGGTDTLTISRLEPEDFAVYYCQYQYNSRWTFEQGTKEIK 107
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RESULT 14
ID PCT-US95-08743-100 STANDARD: PR7; 104 AA.
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XX xxxxxx
XX AC
XX AC
XX 01-JAN-1900
XX
XX
XX Sequence 100, Application PC/TUS9508743.
DE
CC Sequence 100, Application PC/TUS9508743
CC GENERAL INFORMATION:

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CC APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA: US 08/276,852
CC APPLICATION NUMBER:
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 100:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 104 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 104 AA; 11367 MW; 58892 CN;

Query Match      87.9%   Score 670; DB 13; Length 104;
Best Local Similarity 90.3%; Pred. No. 2,90e-44;
Matches          93; Conservative       7; Mismatches    3; Indels     0; Gaps

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Db      61 GSGGDFTLITLSRLEPEDFAVYQCXYGNSVTFFGGTKLEIK 103
QY      65 GSGGDFTLITLSRLEPEDFAVYQCXYGNSVTFFGGTKVEIK 107
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ID      US-08-276-852-100 STANDARD; PRT: 104 AA.
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DT      01-JAN-1900
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XX Sequence 100, Application "US/08276852."
DE
DE Sequence 100, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10656 Nc. 56213eth Torrey Pines Road, Suite 220.
CC CITY: Mail Drop IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
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CC APPLICATION NUMBER: US 08/178,302  
 CC FILING DATE: 30-SEP-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/954,148  
 CC FILING DATE: 30-SEP-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Fitting, Thomas  
 CC REGISTRATION NUMBER: 34,163  
 CC REFERENCE/DOCKET NUMBER: SC1452P  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 619-554-2937  
 CC TELEFAX: 619-554-6312  
 CC INFORMATION FOR SEQ ID NO: 100:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 104 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 104 AA: 11367 MW: 58892 CN;  
 SQ  
 Query Match 87.9%; Score 670; DB 7; Length 104;  
 Best Local Similarity 90.3%; Pred. No. 2.90e-44;  
 Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 Db 1 QSPGTLSPGERATLSGRASQSLNNYLAWYQKPGQAPRLIYGSSTRATGIPDRFSG 60  
 QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 GSGGDTFTLTISRLEPEDFVYVYCOQYQYNSVYTFGQGTKEIK 103  
 QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 65 GSGGDTFTLTISRLEPEDFVYVYCOLYGNRWTFGQGTKEIK 107

Search completed: Tue Feb 24 07:44:57 1998  
 Job time : 13 secs.



\*\*\*\*\*

W P R E H

(TM)

\*\*\*\*\*

Release 2.1D John F. Collins, BioComputing Research Unit  
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Distribution rights by IntelliGenetics, Inc.

MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:18:21 1998. MaxPir time 6.66 seconds

Tabular output not generated. 223,141 Million cell updates/sec

Title: >US-08-844-215-8

Description: (1-107) from US08844215.pep

Perfect Score: 762

Sequence: 1 AELTSPGTLSTLSPGFPRATL.....QQLVNSPWTFGQGIKVEIK 107

Scoring table: PAM 150

Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 29.906; Variance 166.360; scale 0.180

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	697	91.5	108	10	Anti-HIV gp120 immuno	1.57e-42
2	697	91.5	108	19	VL region of HIV neut	1.57e-42
3	594	91.1	129	7	VL region of HIV neut	2.64e-42
4	685	89.9	107	10	Anti-HIV gp120 immuno	1.25e-41
5	685	89.9	107	19	VL region of HIV neut	1.25e-41
6	684	89.8	108	19	VL region of HIV neut	1.50e-41
7	684	89.8	108	9	Anti-HIV gp120 immuno	1.50e-41
8	684	89.8	109	10	Light chain of Amb al	1.50e-41
9	683	89.6	109	9	HSV glycoprotein F b1	1.78e-41
10	680	89.2	109	19	VL of Fab, DL 41 19,	3.00e-41
11	680	89.2	109	10	Anti-HIV gp41 immunog	3.00e-41
12	673	88.3	107	7	Human lambda light ch	1.01e-40
13	670	87.9	104	19	VL region of HIV neut	1.70e-40
14	670	87.9	104	9	Anti-HIV gp120 immuno	1.70e-40
15	670	87.9	111	19	VL of Fab, GL 41 1, b	1.70e-40
16	670	87.9	111	10	Anti-HIV gp41 immunog	1.70e-40
17	662	86.9	108	19	VL region of HIV neut	6.78e-40
18	562	85.9	129	7	F105VK-F105VK	6.79e-40
19	560	85.6	214	19	Ulceraive colitis-as	9.59e-40
20	559	85.5	129	7	F105VK-F105VK	1.14e-39

21	656	86.1	107	10	R54308	Anti-HIV gp120 immuno	1.92e-39
22	656	86.1	107	19	W01266	VL region of HIV neut	1.92e-39
23	656	86.1	134	20	W1155	Anti-lung tumour anti	2.28e-39
24	655	86.0	108	10	R54309	Anti-HIV gp120 immuno	2.28e-39
25	652	85.6	134	22	W24539	Immunoglobulin r101-2	3.83e-39
26	652	85.6	215	19	W07616	Ulceraive colitis-as	3.83e-39
27	641	84.1	108	10	R54355	Anti-HIV gp120 immuno	2.57e-38
28	641	84.1	108	19	W01275	VL region of HIV neut	2.57e-38
29	641	84.1	109	9	P50218	HSV glycoprotein F b1	2.57e-38
30	636	83.5	108	19	W01267	VL region of HIV neut	6.10e-38
31	628	82.4	107	10	R54365	Anti-HIV gp120 immuno	2.43e-37
32	628	82.4	107	19	W01297	VL region of HIV neut	2.43e-37
33	626	82.2	100	5	R25324	Lv region of human rh	3.44e-37
34	626	82.2	112	10	P54379	Anti-HIV 9841 immuno	3.44e-37
35	626	82.2	112	19	W01324	VL of Fab, SS 41 8, b	3.44e-37
36	625	82.0	116	11	R62330	Human V-kappa vk65.8	4.09e-37
37	625	82.0	116	20	W03948	DNA fragment vk65.8,	4.09e-37
38	625	82.0	116	7	R38650	Human V-kappa fragmen	4.09e-37
39	623	81.8	108	10	P54309	Anti-HIV gp120 immuno	5.78e-37
40	620	81.4	107	19	W01294	VL region of HIV neut	9.70e-37
41	620	81.4	107	9	R54325	Anti-HIV gp120 immuno	9.70e-37
42	620	81.4	107	18	W01295	VL region of HIV neut	9.70e-37
43	618	81.1	104	19	W01271	VL region of HIV neut	1.37e-36
44	618	81.1	104	9	R54313	Anti-HIV gp120 immuno	1.37e-36
45	617	81.0	107	9	R54326	Anti-HIV gp120 immuno	1.53e-36

## ALIGNMENTS

RESULT 1  
ID R54307 standard; protein; 108 AA.  
AC R54307;  
DT 10-NOV-1994 (first entry)  
DE Anti-HIV gp120 immunoglobulin light chain variable region b24.  
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain;  
KW variable region; framework; complementarity determining region.  
OS Homo sapiens

FT Key Location/Qualifiers

FT Region 1..21  
FT /label= FR1  
FT Region 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT Region 49..55  
FT /label= CDR2  
FT Region 56..87  
FT /label= FR3  
FT Region 88..95  
FT /label= CDR3  
FT Region 97..108  
FT /label= FR4

PN W9407922-A.  
PD 14-APR-1994.  
PF 30-SEP-1993. U093328.  
PR 30-SEP-1992; US-954148.  
PA (SCRI ) SCRIPPS RES INST.  
PI Barbas CF, Burton DR, Lerner RA;  
DR WPI: 94-135516/16.  
PT New human monoclonal antibodies neutralising HIV - react with  
PT gp120 or gp41 and nucleic acid encoding them; useful for in vivo  
PT or in vitro diagnosis and for passive immuno-therapy  
PS Example, Page 177-178, 248pp, English.  
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
CC amplification using primers specific for heavy and light chain  
CC variable regions. The amplification products were inserted into a  
CC diastronic vector to produce a library of fragments. E.coli XL1  
CC Blue cells were transformed with the library. Filamentous phage were  
CC produced which expressed the MAB regions on their surface. Panning  
CC with gp120 and gp41 resulted in the recovery of immunoreactive  
CC clones. The light chain VK region sequence p54307 is from a gp120-  
CC specific clone.

SQ Sequence 108 AA:

Query Match 91.5%: Score 697; DB 10; Length 108;  
Best Local Similarity 92.5%: Pred. No. 1.57e-42;  
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltspsgtlslsperatlscrasqvisnlylawyqkqpgaprrlllygvsratgipdr 60  
|||||  
QY 2 ELTSPGTLSPGERATLSCRASQVSSSNLYAWYQRPQAPRLLIYGASSPATGIPDP 61  
|||||  
Db 61 fsgsgsgtdftltisrlepedfavyycqgygtspwtfgggtkveik 106  
|||||  
QY 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGQTKVEIK 107  
|||||

RESULT 2

ID W01265 standard; Protein; 108 AA.

AC W01265;  
DE 28-JAN-1997 (first entry)  
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;  
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;  
KW anti-HIV antibody; detection; HIV infection.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FR1  
FT Region 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT Region 49..55  
FT /label= CDR2  
FT Region 56..87  
FT /label= FR3  
FT Region 88..96  
FT /label= CDR3  
FT Region 97..108  
FT /label= FR4  
FT /label= FR4  
PN W09602273-A1.  
PD 01-FEB-1996.

PF 11-JUL-1995; U08743.  
PR 18-JUL-1994; US-276852.  
PA (SCR1) SCRIPPS RES INST.  
PI Barbas CF, Burton DR, Lerner PA;  
DR WPI: 96-179601/18.  
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in  
passive immunotherapy and detection of HIV infection.  
PS Example; Fig 11; 366pp: English.  
CC The sequences given in W01261-92 represent the light chain variable  
regions (VL) of a series of monoclonal antibodies (MAB's) which are  
immunoreactive with HIV glycoprotein gp120 and are capable of  
neutralising HIV. This sequence represents the sequence of the JKI  
gene clone, b24. A MAB containing this VL sequence has the capacity  
to reduce HIV infectivity titre in an in vivo virus infectivity assay  
by 50 % at a concentration of less than 700 ng of antibody/ml, and  
CC binds mature gp120 preferentially over the precursor gp160. The MAB  
CC may be used for determining immunocompetence of a human anti-HIV  
antibody and in the detection of HIV infection  
SQ Sequence 108 AA;

Query Match 91.5%: Score 697; DB 19; Length 108;  
Best Local Similarity 92.5%: Pred. No. 1.57e-42;  
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltspsgtlslsperatlscrasqvisnlylawyqkqpgaprrlllygvsratgipdr 60  
|||||  
QY 2 ELTSPGTLSPGERATLSCRASQVSSSNLYAWYQRPQAPRLLIYGASSPATGIPDP 61  
|||||  
Db 61 fsgsgsgtdftltisrlepedfavyycqgygtspwtfgggtkveik 106  
|||||  
QY 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGQTKVEIK 107  
|||||

RESULT 3

ID R38672 standard; Protein; 129 AA.

AC R38672;  
DE 01-NOV-1993 (first entry)  
DE VK325-JK2.  
KW Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;  
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;  
KW chain; epitope; immune deficiency.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= sig\_peptide  
FT Protein 21..129  
FT /label= mat\_protein  
FT Region 1..116  
FT /label= vk325  
FT Region 117..129  
FT /label= JK2  
FT Region 44..55  
FT /label= CDR1  
FT Region 71..77  
FT /label= CDR2  
FT Region 110..117  
FT /label= CDR3

FT Misc-difference 1  
FT /note= "Met encoded by ATC (sic)"  
FT Misc-difference 35  
FT /note= "Pro encoded by GCA (sic)"  
FT Misc-difference 99  
FT /note= "Leu encoded by GTG (sic)"  
FT Misc-difference 113  
FT /note= "Gly encoded by GAT (sic)"  
FT Misc-difference 114  
FT /note= "Ser encoded by AAC (sic)"  
FT Misc-difference 116  
FT /note= "Pro encoded by GTT (sic)"  
PN W09312232-A.  
PD 24-JUN-1993.  
PF 10-DEC-1992; U10928.  
PR 10-DEC-1991; US-804652.  
PA (DAND) DANA FARRER CANCER INST INC  
PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.  
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;  
DR WPI: 93-214174/26.  
DR N-PSDB: Q42706.  
PT DNA segments encoding monoclonal antibody - which binds to gp120  
and neutralises HIV, for treating AIDS, and for diagnosing and  
PT monitoring HIV infection  
PS Disclosure; Page 74-75; 109pp: English.  
CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from  
other F105 VK sequences given elsewhere in the specification) was  
CC compared with germline gene Humvk325 (Q42706), showing 97.7%  
CC similarity. By nucleotide sequence analysis, F105 appears to  
CC be derived from a member of the VK III subgroup gene family.  
SQ Sequence 129 AA;

Query Match 91.1%: Score 694; DB 7; Length 129;  
Best Local Similarity 93.3%: Pred. No. 2.54e-42;  
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltsgpgtlslsperatlscrasqvisnlylawyqkqpgaprrlllygvsratgipdr 83  
|||||  
QY 3 LTGSPGTLSPGERATLSCRASQVSSSNLYAWYQRPQAPRLLIYGASSPATGIPDP 82  
|||||

Db 84 ssgsgsgtdftltisrlepedfavyycqgygtspwtfgggtkveik 128  
|||||  
QY 63 SSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGQTKVEIK 107  
|||||

RESULT 4

ID R54311 standard; protein; 107 AA.

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AC * R54311;
DE 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 97..107
FT /label= FR4
FT Region 108..110
FT /label= FR5
PN WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1993; US-954148.
PA (SCRI ) SCRI:PPS RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/15.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 180; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC diazotronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54311 is from a gp120-
CC specific clone
CC Sequence 107 AA:
SQ
Query Match 89.9%; Score 685; DB 10; Length 107;
Best Local Similarity 89.6%; Prod No 1 25e-41;
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 1 eltsqptslsperatlscrasqslsnnylawyqgkqgqaprllyssstrgtgipdr 60
QY 2 ELTOSPTLSLSPGEPATLSCPASQSVSSNYLAWYQGPPTQAPRLIYGASSPATGIPDR 61
Db 61 fsggsgtdftltisrlepedfavyvcqhygnsvytfggqtkleik 106
QY 62 FSGSGSGTDFLTLSRLEPEDFAVYVCQLYGNRWTFGGQTKVEIK 107

RESULT 5
ID WO1269 standard; Protein; 107 AA.
AC WO1269;
DE 28-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone B20.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
FT Region 109..110
FT /label= FR5
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 11-JUL-1995; US-276852.

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FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88 96
FT /label= CDR3
FT Region 98..107
FT /label= FR4
FT Region 108..110
FT /label= FR5
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRI:PPS RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example: Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA:
Query Match 89.9%; Score 685; DB 19; Length 107;
Best Local Similarity 89.6%; Prod No 1 25e-41;
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 1 eltsqptslsperatlscrasqslsnnylawyqgkqgqaprllyssstrgtgipdr 60
QY 2 ELTOSPTLSLSPGEPATLSCPASQSVSSNYLAWYQGPPTQAPRLIYGASSPATGIPDR 61
Db 61 fsggsgtdftltisrlepedfavyvcqhygnsvytfggqtkleik 106
QY 62 FSGSGSGTDFLTLSRLEPEDFAVYVCQLYGNRWTFGGQTKVEIK 107

RESULT 6
ID WO1278 standard; Protein; 108 AA.
AC WO1278;
DE 29-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone b6.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
FT Region 109..110
FT /label= FR5
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.

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PA (SCRI) SCRIPPS RES INST.  
 PI Barbas CF, Burton DP, Lerner PA;  
 DR WPI: 96-179601/18.  
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in  
 PT passive immunotherapy and detection of HIV infection  
 PS Example; Fig 11: 36pp; English.  
 CC The sequences given in W01261-92 represent the light chain variable  
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are  
 CC immunoreactive with HIV glycoprotein gp120 and are capable of  
 CC neutralising HIV. This sequence represents the sequence of the JK2  
 CC gene clone, b6. A MAB containing this VL sequence has the capacity  
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay  
 CC by 50 % at a concentration of less than 700 ng of antibody/mL, and  
 CC binds mature gp120 preferentially over the precursor gp160. The MAB  
 CC may be used for determining immunocompetence of a human anti-HIV  
 CC antibody and in the detection of HIV infection.  
 SQ Sequence 108 AA;

Query Match 89.8%; Score 684; DB 19; Length 108;  
 Best Local Similarity 88.7%; Pred. No. 1.50e-41;  
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltspgtltslsperatlscragssissnylawyqgkpgqaprrliygasnratgipdr 60  
 |||||  
 Qy 2 ELTQSPGTLTSLSPGERATLSCRASQSVSSNYLAWYQGPQAPRLLIYGASSRATGIPDR 61  
 |||||

Db 61 fsgsgsgtdftltisrlepedfavyycqgyspytfqggtqldik 106  
 |||||  
 Qy 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGKTKEIK 107  
 |||||

RESULT 7  
 ID R54316 standard; protein; 108 AA.  
 AC R54316;  
 DT 10-NOV-1994 (first entry)  
 DE Anti-HIV gp120 immunoglobulin light chain variable region b6.  
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
 KW neutralisation; monoclonal antibody; kappa light chain;  
 KW variable region; framework; complementarity determining region.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 1..21  
 FT /label= FR1  
 FT Region 22..33  
 FT /label= CDR1  
 FT Region 34..48  
 FT /label= FR2  
 FT Region 49..55  
 FT /label= CDR2  
 FT Region 56..87  
 FT /label= FR3  
 FT Region 88..96  
 FT /label= CDR3  
 FT Region 97..108  
 FT /label= FR4  
 FN W09407922-A.  
 PD 14-APR-1994.  
 PF 30-SEP-1993; U09328.  
 PR 30-SEP-1992; US-954148.  
 PA (SCRI) SCRIPPS RES INST.  
 PI Barbas CF, Burton DP, Lerner PA;  
 DR WPI: 94-135516/16.  
 PT New human monoclonal antibodies neutralising HIV - react with  
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
 PT or in vitro diagnosis and for passive immuno-therapy  
 PS Example; Page 186: 24pp; English.  
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
 CC amplification using primers specific for heavy and light chain  
 CC variable regions. The amplification products were inserted into a  
 CC dicistronic vector to produce a library of fragments. E.coli XL1  
 CC blue cells were transformed with the library. Filamentous phage were  
 CC produced which expressed the MAB regions on their surface. Panning  
 CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence R54316 neutralises HIV1  
 CC gp120  
 SQ Sequence 108 AA;

Query Match 89.8%; Score 684; DB 9; Length 108;  
 Best Local Similarity 88.7%; Pred. No. 1.50e-41;  
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltspgtltslsperatlscragssissnylawyqgkpgqaprrliygasnratgipdr 60  
 |||||  
 Qy 2 ELTQSPGTLTSLSPGERATLSCRASQSVSSNYLAWYQGPQAPRLLIYGASSRATGIPDR 61  
 |||||

Db 61 fsgsgsgtdftltisrlepedfavyycqgyspytfqggtqldik 106  
 |||||  
 Qy 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGKTKEIK 107  
 |||||

RESULT 8  
 ID R56286 standard; protein; 109 AA.  
 AC R56286;  
 DT 04-MAR-1995 (first entry)  
 DE Light chain of Amb al-specific IgG4 antibody.  
 KW Allergen-specific immunoglobulin A; IgA; AL 15-5.2; light chain;  
 KW allergen Amb a 1; ragweed; Ambrosia elator.  
 OS Synthetic.  
 PN W09414475-A.  
 PD 07-JUL-1994.  
 PF 20-DEC-1993; W12501  
 PR 21-DEC-1992; US-994126.  
 PA (TANO-) TANOX BIOSYSTEMS INC.  
 PI Chang TW;  
 DR WPI: 94-234353/28.  
 DR N-PSDB: Q66538.  
 PT Compsn. contg. allergen specific IgA for treating mucosal tissue  
 PT - and conjugates of allergen specific Ig with polymer, for  
 PT treating IGE mediated allergies and for isolation of specific  
 PT allergens  
 PS Example; Page 27-28: 36pp; English.  
 CC Blood samples were collected from patients immunised with allergens  
 CC including ragweed (Ambrosia elator) extracts. The dominant allergen  
 CC in short ragweed is Amb a 1. Purified PBLs were immortalised and  
 CC then fused with mouse myeloma cell line 653 and the resultant clones  
 CC were screened using Amb a 1 protein. A single cell subclone AL 16-5.2,  
 CC secreting Amb al-specific IgG4, kappa antibody was selected. Total  
 CC RNA was prep'd. from the AL 16-5.2 cells and first strand cDNA was  
 CC pred. using oligo dT primers. When the first strand cDNA was used as  
 CC the template, and the 5' and 3' kappa light chain primers (Q66540,  
 CC Q66541) were used in PCR and amplified band of the expected size was  
 CC noted. The DNA sequence of several subclones contg. this amplified  
 CC DNA fragment was determined. The sequence and its deduced AA  
 CC sequence are shown in Q66538 and R56286. Comparison of the deduced  
 CC AL 16-5.2 L-chain sequence with human V region sequences indicates  
 CC that it is a member of the human VK III subgp.  
 SQ Sequence 109 AA;

Query Match 89.8%; Score 684; DB 10; Length 109;  
 Best Local Similarity 87.6%; Pred. No. 1.50e-41;  
 Matches 92; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltsgsgtdftltisrlepedfavyycqgyspytfqggtqldik 108  
 |||||  
 Qy 3 LTQSPGTLTSLSPGERATLSCRASQSVSSNYLAWYQGPQAPRLLIYGASSRATGIPDR 62  
 |||||

Db 64 tsgsgsgtdftltisrlepedfavyycqgyspytfqggtqldik 108  
 |||||  
 Qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGKTKEIK 107  
 |||||

RESULT 9  
 ID R50217 standard; protein; 109 AA.  
 AC R50217;  
 DT 31-OCT-1994 (first entry)  
 DE HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.

KW Complementarity determination region: CDR3: human; bronchiolitis;  
 KW monoclonal antibody; epitope; glycoprotein F; influenza virus;  
 KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;  
 OS Lung; pneumonia.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT Region 24..35  
 FT /label= CDR1  
 FT Region 36..50  
 FT /label= FR2  
 FT Region 51..57  
 FT /label= CDR2  
 FT Region 58..89  
 FT /label= FR3  
 FT Region 90..94  
 FT /label= CDR3  
 FT Region 94..109  
 FT /label= FR4  
 PN WO9406448-A.  
 PD 31-MAR-1994.  
 PF 16-SEP-1993: U08786.  
 PR 16-SEP-1992: US-945515.  
 PA (USSH ) SCRIPPS RES INST.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI Barbas CF, Burton DR, Chanock PM, Crowe JE, Murphy RP,  
 DR WPI: 94-118147/14.  
 PT Human neutralising monoclonal antibodies to respiratory syncytial  
 PT virus - for treatment prophylaxis and diagnosis of PSV and other  
 PT diseases of the respiratory tract  
 PS Disclosure: Fig 4: 104pp; English.  
 CC The sequences given in R50215-19 represent the heavy and light chain  
 CC variable domains of various clones of a human monoclonal antibody  
 CC which binds to an epitope on glycoprotein F of respiratory syncytial  
 CC virus (RSV). These antibodies may be used as a reagent for the  
 CC diagnosis of RSV disease and other viral mucosal diseases, eg.  
 CC influenza virus, rhinovirus and coronavirus. They are particularly  
 CC useful in ameliorating RSV when delivered directly to the lungs, and  
 CC may also be used for treating pneumonia and bronchiolitis.  
 SQ Sequence 109 AA;

Query Match 89.6%; Score 683; DB 9; Length 109;  
 Best Local Similarity 89.7%; Pred. No. 1.78e-41;  
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 2 aeltspgtlslspgeratlsratqssnylawyqgqgqprlllycasratdtd 61  
 QY 1 AELTSPGTLSLSPGERATLSRATQSSVSSNYLAWYQGPDPAPPLLIYGASSPATGIPD 60  
 Db 62 rfsgsgtdftltisrlepedfamyvqdydispytfgggtkveik 108  
 QY 61 RFSGSGTDTFTLTISRLEPEDFAVYVCQLYGNRSRWTFGGGTKEIK 107

RESULT 10  
 ID WO1320 standard: Protein: 109 AA.  
 AC WO1320:  
 DE 29-JAN-1997 (first entry)  
 DE VL of Fab, DL 41 19, binds to HIV gp41.  
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;  
 KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
 KW virus infectivity assay; precursor gp150; immunocompetence; human;  
 KW anti-HIV antibody; detection; HIV infection.  
 OS Homo sapiens.

FT Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT Region 24..35  
 FT /label= CDR1  
 FT Region 36..50  
 FT /label= FR2  
 FT Region 51..57

FT /label= CDR2  
 FT Region 58..89  
 FT /label= FR3  
 FT Region 90..97  
 FT /label= CDR3  
 FT Region 98..109  
 FT /label= FR4  
 PN WO9602273-A1.  
 PD 01-FEB-1996.  
 PF 11-JUL-1995: U08743.  
 PA 18-JUL-1994: US-276852  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI: 96-179601/18.  
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in  
 PT passive immunotherapy and detection of HIV infection.  
 PS Example 1: Fig 1a: 35pp; English.  
 CC The sequences given in WO1320-24 represent the light chain variable  
 CC regions (VH) of a series of antibody fragments (FAB's) which are  
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents  
 CC the sequence of the clone, DL 41 19. These sequences represent light  
 CC chains which bind to the heavy light chain clones given in WO1315-19. A  
 CC monoclonal antibody containing one of these Fab sequences may have the  
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity  
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.  
 CC The MAb may be used for determining immunocompetence of a human anti-HIV  
 CC antibody and in the detection of HIV infection.  
 SQ Sequence 109 AA;

Query Match 89.2%; Score 680; DB 19; Length 109;  
 Best Local Similarity 91.6%; Pred. No. 3.00e-41;  
 Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltspgtlslspgeratlsratqssnylawyqgqgqprlllycasratdtd 61  
 QY 1 AELTSPGTLSLSPGERATLSRATQSSVSSNYLAWYQGPDPAPPLLIYGASSPATGIPD 60  
 Db 62 rfsgsgtdftltisrlepedfamyvqdydispytfgggtkveik 107  
 QY 61 RFSGSGTDTFTLTISRLEPEDFAVYVCQLYGNRSRWTFGGGTKEIK 107

RESULT 11  
 ID R54275 standard: protein: 109 AA.  
 AC R54275;

DE 10-NOV-1994 (first entry)  
 DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.  
 KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;  
 KW neutralisation; monoclonal antibody; light chain; variable region;  
 KW framework region; complementarity determining region.

OS Homo sapiens.  
 FT Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT Region 24..35  
 FT /label= CDR1  
 FT Region 36..50  
 FT /label= FR2  
 FT Region 51..57  
 FT /label= CDR2  
 FT Region 58..89  
 FT /label= FR3  
 FT Region 90..97  
 FT /label= CDR3  
 FT Region 98..109  
 FT /label= FR4  
 PN WO9407922-A.  
 PD 14-APR-1994.

PF 30-SEP-1993: U09328.  
 PR 30-SEP-1992: US-954148.  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI: 94-135616/16.

PT New human monoclonal antibodies neutralising HIV - react with  
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
PT or in vitro diagnosis and for passive immuno-therapy  
PS Claim 11; Page 215-216; 248pp; English.  
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
CC amplification using primers specific for heavy and light chain  
CC variable regions. The amplification products were inserted into a  
CC dicistronic vector to produce a library of fragments. E.coli XL1  
CC Blue cells were transformed with the library. Filamentous phage were  
CC produced which expressed the MAB regions on their surface. Panning  
CC with gp120 and gp41 resulted in the recovery of immunoreactive  
CC clones. The light chain VL region sequence R54275 neutralises HIV1  
CC gp41.  
SQ Sequence 109 AA;

Query Match 89.2%; Score 680; DB 10; Length 109;  
Best Local Similarity 91.6%; Pred. No. 3,00e-41;  
Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipd 61  
QY 1 aeltspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipd 60  
Db 62 rfsgsgtdftltisrlepedfavyycqygssg-tfgggtkveik 107  
QY 61 rfsgsgtdftltisrlepedfavyycqygssg-tfgggtkveik 107

RESULT 12  
ID R38593 standard; peptide; 107 AA.  
AC R38593;  
DT 28-OCT-1993 (first entry)  
DE Human lambda light chain subgroup 3 (hL3).  
KW Antibody; variable domain; light; L; heavy; H; consensus;  
KW affinity; antigen; immunogenicity; humanisation; framework.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc\_difference 96  
FT /note- "residue conserved in less than 50% of the  
FT known sequences of hL3"  
FT W09311794-A.  
PD 24-JUN-1993.  
PF 14-DEC-1992; U10906.  
PR 13-DEC-1991; US-808464.  
PA (XOMA) XOMA CORP.  
PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;  
DR WPI, 93-213827/26.  
CC Antibodies prepn. used for treatment of auto-immune diseases - by  
CC replacement of critical residues to reduce immunogenicity but  
CC retain binding affinity, etc.  
PS Claim 2; Page 93-94; 160pp; English.  
CC The consensus amino acid sequences for the subgroups of light  
CC chains (hK1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -  
CC R38592, hL3 - R38593, hL5 - R38594, hK4 - R38595, hL4 - R38596,  
CC and hU5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and  
CC hH2 - R38600) of human variable domains may be used to prepare, for  
CC example, a modified mouse antibody variable domain that retains the  
CC affinity of the natural domain for antigen while exhibiting reduced  
CC immunogenicity in humans.  
CC Unlike other methods of humanisation, which advocate the  
CC replacement of entire antibody framework regions with those of human  
CC antibodies, this method involves only the introduction of human  
CC residues into those positions not critical for antigen binding.  
CC This ensures that the binding properties of the modified antibody  
CC are not diminished.  
SQ Sequence 107 AA;

Query Match 88.3%; Score 673; DB 7; Length 107;  
Best Local Similarity 92.4%; Pred. No. 1.01e-40;  
Matches 97; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 4 ltqspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipdf 62  
QY 1 ltqspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipdf 61

QY 3 LIQSPGTLSPGKATLSCKASQSVSSNYLAWYQKPGQAPRLLYGASSNAIUIPDRF 62  
Db 63 sgsgsgtdftltisrlepedfavyycqygssgxtfsggtdvveik 107  
QY 63 sgsgsgtdftltisrlepedfavyycqygssgxtfsggtdvveik 107

RESULT 13  
ID W01279 standard; protein; 104 AA.  
AC W01279;  
DT 29-JAN-1997 (first entry)  
DE VL region of HIV neutralising MAB, clone s6.  
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;  
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;  
KW anti-HIV antibody; detection; HIV infection.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..18  
FT /label= FR1  
FT Region 19..30  
FT /label= CDR1  
FT Region 31..45  
FT /label= FR2  
FT Region 46..52  
FT /label= CDR2  
FT Region 53..84  
FT /label= FR3  
FT Region 85..93  
FT /label= CDR3  
FT Region 94..104  
FT /label= FR4  
PN W09602273-A1.  
PD 01-FEB-1996.  
PF 11-JUL-1995; 008743.  
PR 18-JUL-1994; US-276852.  
PA (SCPI) SCRIPPS RES INST  
PI Barbas CF, Burton DR, Lerner RA;  
DR WPI, 96-179601/18.  
PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in  
PT passive immuno-therapy and detection of HIV infection.  
PS Example; Fig 11; 366pp; English.  
CC The sequences given in W01261-92 represent the light chain variable  
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are  
CC immunoreactive with HIV glycoprotein gp120 and are capable of  
CC neutralising HIV. This sequence represents the sequence of the JK2  
CC gene clone, s6. A MAB containing this VL sequence has the capacity  
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay  
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and  
CC binds mature gp120 preferentially over the precursor gp160. The MAB  
CC may be used for determining immunocompetence of a human anti-HIV  
CC antibody and in the detection of HIV infection.  
SQ Sequence 104 AA;

Query Match 87.9%; Score 670; DB 19; Length 104;  
Best Local Similarity 90.3%; Pred. No. 1.70e-40;  
Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 1 qspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipdfsg 60  
QY 5 qspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipdfsg 64  
Db 61 gsgsgtdftltisrlepedfavyycqygssgxtfsggtdvveik 103  
QY 65 sgsgsgtdftltisrlepedfavyycqygssgxtfsggtdvveik 107

RESULT 14  
ID R54317 standard; protein; 104 AA.  
AC R54317;  
DT 10-NOV-1994 (first entry)  
DE Anti-HIV gp120 immunoglobulin light chain variable region s6.  
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

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KW neutralisation: monoclonal antibody: kappa light chain;
KW variable region: framework: complementarity determining region
OS Homo sapiens.
FH Key Location/Qualifiers
FT /label= FR1 1..18
FT /label= FR2 19..30
FT /label= CDR1 31..45
FT /label= FR2 46..52
FT /label= CDR2 53..84
FT /label= FR3 85..93
FT /label= CDR3 94..104
FT /label= FR4 105..118
PN W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCR1 ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 186-187; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which were screened with the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54317 neutralises HIV1
CC gp120.
SQ Sequence 104 AA:

Query Match 87.9%; Score 670; DB 9; Length 104;
Best Local Similarity 90.3%; Pred No 170e-40;
Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 1 qspgtlslspgeratlsrscasqsvsngylawygkqkqgqprlllygsstratgipdrfsq 60
   |||||
QY 5 QSPGTLSPGCEATLSRPSQSVSSNYLAWYQPPGQAPPELLIYGASSRATGIPDRFSG 64

Db 61 gsgtdftltisrlepedfavyycqyqnsyvtfggqtkleik 103
   :|||||
QY 65 SGSGTDFTLTISRLEPEDFAVYVCQLYGNRPWFQGGTKVEIK 107

RESULT 15
ID W01322 standard; Protein: l1l AA.
AC W01322;
DE 29-JAN-1997 (first entry)
DE VL of Fab, GL 41, binds to HIV gp41.
KW Heavy chain; light chain; variable region, VH, monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT /label= FR1 1..23
FT /label= FR2 24..35
FT /label= CDR1 36..50
FT /label= FR2 51..57
FT /label= CDR2 58..89
FT /label= FR3 90..97
FT /label= CDR3 98..111
FT /label= FR4 112..118
PN W09602373-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCR1 ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example 3; Fig 19; 366pp; English.
CC The sequences given in W01320-24 represent the light chain variable
CC regions (VH) of a series of antibody fragments (FAB's) which are
CC immunoreactive with HIV glycoprotein gp41. This sequence represents
CC the sequence of the clone, GL 41. These sequences represent light
CC chains which bind to the heavy light chain clones given in W01315-19. A
CC monoclonal antibody containing one of these Fab sequences may have the
CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
CC assay by 50 % at a concentration of less than 700 ng of antibody/ml
CC The MAB may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 111 AA;

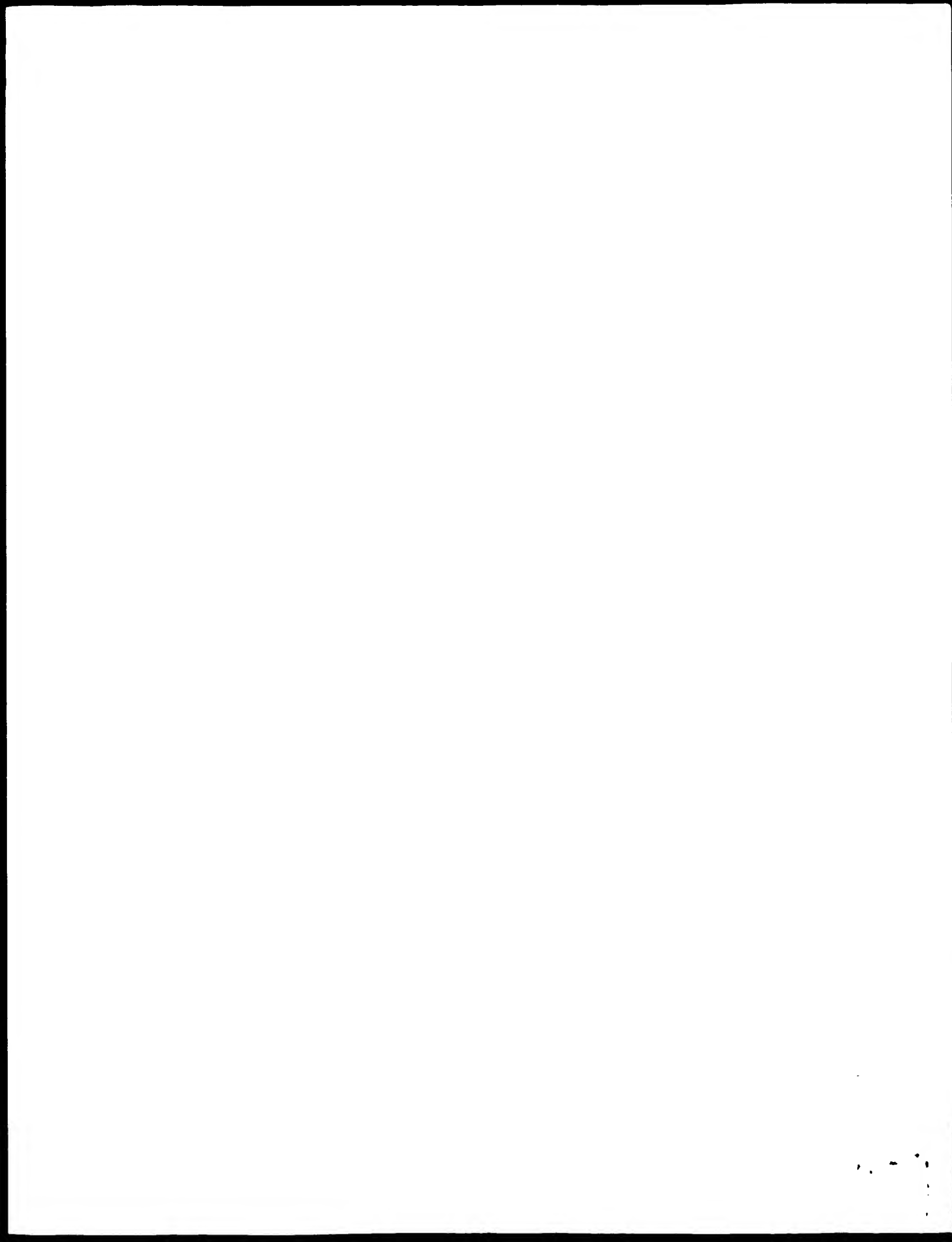
Query Match 87.9%; Score 670; DB 19; Length 111;
Best Local Similarity 87.9%; Pred No 1.70e-40;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltspstlslpgeratlsrscasqsvsngylawygkqkqgqprlllygsstratgipdr 61
   |||||
QY 1 AELTSPGTLSPGCEATLSRPSQSVSSNYLAWYQPPGQAPPELLIYGASSRATGIPDR 60

Db 62 rfsgsgsqaadtltisrlepedfavyycqyqagsh-tfggqtkleik 107
   |||||
QY 61 PFSGSGSGTDTLTISRLEPEDFAVYVCQLYGNRPWFQGGTKVEIK 107

Search completed: Tue Feb 24 07:18:48 1998
Job time : 27 secs.

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\*\*\*\*\*  
WATERMAN  
\*\*\*\*\* (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Feb 24 07:15:25 1998 MasPar time 5.77 Seconds  
498,040 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-844-215-7  
Description: (1-126) from US08844215.pep  
Perfect Score: 949  
Sequence: 1 EVQLLESGSEVKKPGSSVKV.....GSCWGFDPWGQGLIVTVSS 126

Scoring table: PAM 150  
Gap 11  
Searched: 59021 seqs, 21210388 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11  
Statistics: Mean 41.449; Variance 70.286; scale 0.500

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	591	62.3	117	5	HV1A_HUMAN IG HEAVY CHAIN V-1 PE	1 04e-110
2	532	56.1	117	5	HV1B_HUMAN IG HEAVY CHAIN PRECUR	1 15e-96
3	515	54.3	117	5	HV1G_HUMAN IG HEAVY CHAIN PRECUR	1 21e-92
4	486	51.2	143	5	HV1C_HUMAN IG HEAVY CHAIN PRECUR	8 38e-86
5	478	50.4	125	5	HV1F_HUMAN IG HEAVY CHAIN V-1 PE	5 36e-84
6	470	49.5	114	5	HV0C_MOUSE IG HEAVY CHAIN V-1 PE	4 90e-82
7	454	47.8	140	5	HV02_MOUSE IG HEAVY CHAIN PRECUR	2 68e-78
8	445	47.0	120	5	HV03_MOUSE IG HEAVY CHAIN V-1 PE	1 98e-76
9	445	46.9	120	5	HV03_MOUSE IG HEAVY CHAIN V-1 PE	3 39e-76
10	445	46.9	139	5	HV07_MOUSE IG HEAVY CHAIN PRECUR	3 39e-76
11	441	46.5	118	5	HV51_MOUSE IG HEAVY CHAIN V-1 PE	2 90e-75
12	438	46.2	117	5	HV12_MOUSE IG HEAVY CHAIN V-1 PE	1 45e-74
13	436	45.9	117	5	HV06_MOUSE IG HEAVY CHAIN PRECUR	4 24e-74
14	435	45.8	117	5	HV52_MOUSE IG HEAVY CHAIN PRECUR	7 25e-74
15	434	45.7	117	5	HV53_MOUSE IG HEAVY CHAIN V-1 PE	1 24e-73
16	432	45.5	138	5	HV13_MOUSE IG HEAVY CHAIN PRECUR	3 62e-73
17	431	45.4	117	5	HV14_MOUSE IG HEAVY CHAIN PRECUR	6 18e-73
18	430	45.3	117	5	HV04_MOUSE IG HEAVY CHAIN PRECUR	1 06e-72
19	427	45.0	117	5	HV05_MOUSE IG HEAVY CHAIN PRECUR	5 26e-72
20	419	44.2	117	5	HV49_MOUSE IG HEAVY CHAIN PRECUR	3 79e-70
21	415	43.7	117	5	HV09_MOUSE IG HEAVY CHAIN PRECUR	3 20e-69
22	415	43.7	124	5	HV1Q_HUMAN IG HEAVY CHAIN V-1 PE	3 20e-69

23	414	43.6	122	5	HV2G_HUMAN IG HEAVY CHAIN V-1 PE	5 46e-69
24	408	43.0	121	5	HV01_MOUSE IG HEAVY CHAIN V-1 PE	1 34e-67
25	407	42.9	137	5	HV11_MOUSE IG HEAVY CHAIN PRECUR	2 28e-67
26	405	42.7	117	5	HV1C_MOUSE IG HEAVY CHAIN PRECUR	5 50e-67
27	404	42.6	125	5	HV3K_HUMAN IG HEAVY CHAIN V-1 PE	1 12e-66
28	401	42.3	124	5	HV1E_HUMAN IG HEAVY CHAIN V-1 PE	5 54e-66
29	400	42.1	120	5	HV3U_HUMAN IG HEAVY CHAIN V-1 PE	9 42e-66
30	399	42.0	122	5	HV3H_HUMAN IG HEAVY CHAIN V-1 PE	1 50e-65
31	393	41.4	117	5	HV4C_HUMAN IG HEAVY CHAIN PRECUR	3 87e-64
32	392	41.3	122	5	HV3A_HUMAN IG HEAVY CHAIN V-1 PE	6 58e-64
33	391	41.2	120	5	HV1H_HUMAN IG HEAVY CHAIN V-1 PE	1 12e-63
34	383	40.4	121	5	HV3J_HUMAN IG HEAVY CHAIN V-1 PE	7 42e-62
35	379	39.9	119	5	HV3I_HUMAN IG HEAVY CHAIN V-1 PE	6 40e-61
36	378	39.8	120	5	HV3E_HUMAN IG HEAVY CHAIN V-1 PE	1 08e-60
37	377	39.7	136	5	HV15_MOUSE IG HEAVY CHAIN PRECUR	1 84e-60
38	374	39.4	142	5	HV01_PAT IG HEAVY CHAIN PRECUR	8 95e-60
39	370	39.0	115	5	HV3D_HUMAN IG HEAVY CHAIN V-1 PE	7 37e-59
40	370	39.0	123	5	HV23_MOUSE IG HEAVY CHAIN V-1 PE	7 37e-59
41	368	38.8	117	5	HV03_CAPRA IG HEAVY CHAIN PRECUR	2 11e-58
42	366	38.6	119	5	HV4O_MOUSE IG HEAVY CHAIN V-1 PE	6 05e-58
43	365	38.5	119	5	HV37_MOUSE IG HEAVY CHAIN V-1 PE	1 02e-57
44	364	38.4	114	5	HV3B_HUMAN IG HEAVY CHAIN V-1 PE	1 73e-57
45	364	38.4	119	5	HV38_MOUSE IG HEAVY CHAIN V-1 PE	1 73e-57

ALIGNMENTS

RESULT	1	STANDARD	PRT	117 AA
ID	HV1A_HUMAN			
AC	P01742			
DT	21-JUL-1986 (REL. 01. CREATED)			
DI	21-JUL-1986 (REL. 01. LAST SEQUENCE UPDATE)			
DT	21-JUL-1986 (REL. 01. LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN V-1 REGION (EU)			
OS	HOMO SAPIENS (HUMAN)			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
RP	SEQUENCE.			
RN	[1]			
RX	MEDLINE: 71064024			
RA	CUNNINGHAM R.A., RUTISHAUSER U., GALL W.E., GOTTlieb P.D.,			
PA	WAXDAL M.J., EDELMAN G.M.:			
RL	BIOCHEMISTRY 9:3151-3170(1970).			
RN	[2]			
RP	DISULFIDE BOND.			
RX	MEDLINE: 71064027			
RA	GALL W.E., EDELMAN G.M.:			
PA	BIOCHEMISTRY 9:3188-3196(1970).			
RL	BIOCHEMISTRY 9:3151-3170(1970).			
CC	- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.			
DR	PIR: A02023; GIHEU.			
DP	HSSP: P01810; IFVR			
KW	IMMUNOGLOBULIN V REGION.			
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.			
FT	DISULFD 22 96			
FT	NON_TER 117 117			
SQ	SEQUENCE 117 AA: 12472 MW: 26898170 CRC32:			
Query Match	52.3%	Score 591:	DB 5: Length 117;	
Best Local Similarity	79.0%	Pred. No. 1.04e-110;		
Matches	79: Conservative	11: Mismatches	0: Gaps	0:
Db	1 gqvlgsaevkkgssvkvscasgdtfsrslwvrgpaggglevmqalvfmfpny 60			
Qy	1 EVQLLESGSEVKKPGSSVKVSPASGSGSFSSYNFNNWVRAPGQGLEWMGSLIFPFGIANY 50			
Db	61 aqkfgprtticadstntatymelsslrstafycaggy 100			
Qy	61 AOKFGQRTIITADESTATGYMELSSLRSEDTAVYVCAMPY 100			
RESULT	2	STANDARD	PRT	117 AA
ID	HV1B_HUMAN			

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RESULT 4
ID HV1F_HUMAN STANDARD: PRT; 143 AA.
AC P01744;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
DS HOMO SAPIENS (HUMAN).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83065234.
RA KENTEN J.H., MOUNGAARD H.V., HOUGHTON M., DERBYSHIRE R.B., VINEY J.,
RA BELL L.O., GOULD H.J.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
[2]
SEQUENCE OF 16-142.
RA BENNICH H.H., JOHANSSON S.G.O., VON BAHR-LINDSTROM H.;
RL (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS.
RL BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).
CC -!- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A02036; ELHUND.
DR HSSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 15
FT CHAIN 16 143 IG HEAVY CHAIN V REGION (ND).
FT MOD_RES 16 16 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 37 111
FT CONFLICT 17 17 T -> V (IN REF. 2).
FT CONFLICT 49 50 IH -> HI (IN REF. 2).
FT CONFLICT 63 64 VG -> GV (IN REF. 2).
FT CONFLICT 121 121 MISSING (IN REF. 2).
FT NON_TER 143 143
FT SEQUENCE 143 AA; 16051 MW; 6D605E13 CRC32;

Query Match 51.2%; Score 486; DB 5; Length 143;
Best Local Similarity 54.3%; Pred. No. 8.38e-86;
Matches 70; Conservative 28; Mismatches 27; Indels 4; Gaps

Db 16 qtqlvsgaevrkpgasrvvscasytfldsyhiwraqphglewgvwnpnsqgtny 75
: ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
QY 1 EVOLLESGEVKPGSSVKVSKASGSGSRFNFVNVRAPQGLEWMGGTIPMFGTANY 60
: ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Db 76 aprfgvtrmdrdsafstymdlrsrdsdsafvcskdpdwsdyndfsyt-lgawg 134
: ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
QY 61 AOKTQGRVTITADESTATGMYELSLSRSEDTAVYICAM--PY-PKHCGRSGCWGFDPWG 117
: ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Db 135 ggtvtvtvss 143
: ||| |||||
QY 118 QGTLTVTSS 126
: ||| |||||

RESULT 5
ID HV1F_HUMAN STANDARD: PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (NOT).
DS HOMO SAPIENS (HUMAN).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 86203277.
RA KOJIMA M., KOIDE T., ODANI S., ONO T.;
RL MOL. IMMUNOL. 23:169-174(1986).
DR PIR; A02025; HVHUMO.
DR HSSP; P01772; 8FAB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.

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FT DOMAIN 99 107 D SEGMENT
FT DOMAIN 108 125 J SEGMENT
FT DISULFID 122 96 BY SIMILARITY.
FT NON_TER 125 125
SQ SEQUENCE 125 AA: 13579 MW: 6745023 CRC32:

Query Match 50.4% Score 478 DB 5: Length 125;
Best Local Similarity 50.8% Pred No 5 36e-94;
Matches 68: Conservative 26; Mismatches 35; Indels 1; Gaps 1;

Db 1 qvqlqsgaeivkagssvkmcsksgyftfssygmwvqarqlewmavvhsddrtty 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGSEVKKPGSSVKVSCRASGGSFSPSYNFWVPQAPGCGLEWGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 qprqarftvrdstttvymelcaltsadtaiyycarg-ahysdtdsdslypwwqgt 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AOKFOGRVITADESTATGYMELSLSPSEDTAVYICAMPYKHCSCGSGCWGDFPWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 120 lltvss 125
:|||||:
QY 121 LVTVSS 126

RESULT 6
ID HV00_MOUSE STANDARD: PRT: 114 AA
AC P01741:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (ANTI-APSONATE ANTIBODY).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
CC EUTHERIA: RODENTIA
RN [1]
RP SEQUENCE.
RC STRAIN-A/J;
RX MEDLINE: 79195438.
FA CAPRA J D, NISONOFF A;
RL J. IMMUNOL. 123:279-284(1979).
CC -1- ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IGG1
CC SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
CC SEQUENCE.
DR PIR: A02022; GINSA.
DR HSSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA: 12555 MW: 1A027FID CRC32:

Query Match 49.5% Score 470; DB 5: Length 114;
Best Local Similarity 70.4% Pred No 4 80e-82;
Matches 59: Conservative 17; Mismatches 12; Indels 0; Gaps 0;

Db 1 evqlqsgaeivkagssvkmcsksgyftfssygmwvqarqlewmavvhsddrtty 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGSEVKKPGSSVKVSCRASGGSFSPSYNFWVPQAPGCGLEWGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 aqkfggrvttadestntaymelslrsdsdtavycav 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AOKFOGRVITADESTATGYMELSLSPSEDTAVYICAM 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
ID HV02_MOUSE STANDARD: PRT: 140 AA
AC P01746:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN [1]
RP SEQUENCE FROM N.A.

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PC STRAIN-A/J;
RX MEDLINE: 82152818.
FA SINS J, PARRITIS T H, ESTESS P, SLAUGHTER C, TUCKER P W.
RA CAPRA J D.
P1 SCIENCE 216:309-311(1982).
DP EMBL: J00403; G195007;
DR PIR: A02028; HVMG7.
DR HSSP: P01789; 6FAB.
KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY: HYBRIDOMA: SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
FT NON_TER 140 140
SQ SEQUENCE 140 AA: 0790D5C8 CRC32:

Query Match 47.8% Score 454; DB 5: Length 140;
Best Local Similarity 56.3% Pred. No. 2.68e-78;
Matches 71: Conservative 23; Mismatches 27; Indels 5; Gaps 4;

Db 20 evqlqsgaeivkagssvkmcsksgyftfssygmwvqarqlewmavvhsddrtty 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGSEVKKPGSSVKVSCRASGGSFSPSYNFWVPQAPGCGLEWGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 nekfgkttltvdkssstaysmqlrsltsedsavycarsh--yyg-gs-yd-fdywqgt 134
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AOKFOGRVITADESTATGYMELSLSPSEDTAVYICAMPYKHCSCGSGCWGDFPWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 135 pltvss 140
:|||||:
QY 121 LVTVSS 126

RESULT 8
ID HV50_MOUSE STANDARD: PRT: 120 AA
AC P06329:
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (AC38 15.3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
CC EUTHERIA: RODENTIA
RN [1]
RP SEQUENCE.
RX MEDLINE: 84182519.
RA DILDROP P, ROVENS J, SIEKEVITZ M, REYREUTHIER K, RAJENSKY K.
RL EMBL J. 3:517-523(1984).
DR PIR: A02037; MMS15.
DR HSSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA: 1F311 MW: 85E0C1BA CRC32:

Query Match 47.0% Score 446; DB 5: Length 120;
Best Local Similarity 53.2% Pred. No. 1.98e-76;
Matches 57: Conservative 25; Mismatches 28; Indels 6; Gaps 5;

Db 1 qvqlqsgaeivkagssvkmcsksgyftfssygmwvqarqlewmavvhsddrtty 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGSEVKKPGSSVKVSCRASGGSFSPSYNFWVPQAPGCGLEWGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 nekfkstltvdkssstaysmqlrsltsedsavycarsh--dye-gd-r-yfdwqgt 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AOKFOGRVITADESTATGYMELSLSPSEDTAVYICAMPYKHCSCGSGCWGDFPWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 115 pltvss 120
:|||||:
QY 121 LVTVSS 126

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RESULT 9
ID HV03_MOUSE STANDARD: PRT: 120 AA
AC P01747;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN V REGION (36-65)
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE FROM N.A.
RX MEDLINE: 83131846
RA SIEKEVITZ M., GEFTER M.L., BRODEUR P., PIBLET R.,
RA MARSHAK-ROTHSTEIN A.;
RL EUR J IMMUNOL 12:1023-1032(1982);
CC - FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
CC THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
CC THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
DR PIR: A02028; HYMSG7.
DR HSP: P01789; 6FAB.
KW IMMUNOGLOBULIN V REGION; ANTIPSONATE ANTIBODY; HYBRIDOMA
FT NON_TER 120
SQ SEQUENCE 120 AA; 13307 MW; BBA8CCA1 CRC32;

Query Match
Best Local Similarity 46.9%; Score 445; DB 5; Length 120;
Matches 69; Conservative 25; Mismatches 26; Indels 5; Gaps 5,

Db 1 vqlqsgaelvradssvkmksasgyftsyglnwqkqpgqlewigvnpngdytkyn 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2 VOLLESSEVKKPGSSVKVSCRASGSGFRSYNFNNVQAPGQGLEWMGGLIPMFGTANY 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ekfkgkttlvdkssstymqltsedsavvyfars-v-ygq-gs-y-yfdywgqgtt 115
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 QKFCGRVITTADESTATGYMELSLPSEDATVYVCAMPYKPKHCSGSGWGFNPWQGT 121
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 ltvs 120
|||||
QY 122 VTVS 126
|||||

RESULT 10
ID HV03_MOUSE STANDARD: PRT: 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (R1-8 / 186-2)
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6.
RX MEDLINE: 81234548.
RA BATHWELL A L M., PASKIND M., RETH M., IMANISHI-KAPI T., PAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
CC - THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES).
DR EMBL: J00529; G195115;
DR PIR: A02034; MHMS18.
DR HSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.

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FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 134 H2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139
SQ SEQUENCE 139 AA; 15419 MW; DEB2C7DA CRC32;

Query Match
Best Local Similarity 54.0%; Score 445; DB 5; Length 139;
Matches 68; Conservative 27; Mismatches 25; Indels 6; Gaps 4;

Db 20 qvqlqsgaelvkgasvklscasgyftsywmhwkqrpgrglewlgtrldpnsqtky 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 EVOLLESSEVKKPGSSVKVSCRASGSGFRSYNFNNVQAPGQGLEWMGGLIPMFGTANY 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 nekfkstltvdkssstymqltsedsavvyfars-y-dyy--gs--syfdywgqgtt 133
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AQKFCGRVITTADESTATGYMELSLPSEDATVYVCAMPYKPKHCSGSGWGFNPWQGT 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 134 ltvs 139
|||||
QY 121 LTVSS 126
|||||

RESULT 11
ID HV51_MOUSE STANDARD: PRT: 118 AA.
AC P06330;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DE 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (AC38 205.12).
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE.
RX MEDLINE: 84182519
RA DILDOPEP R., BOVENS J., SIEKEVITZ M., REYEUETHER K., PAJEWSKY K.;
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR HSP: P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 2D1DCE77 CRC32;

Query Match
Best Local Similarity 46.5%; Score 441; DB 5; Length 118;
Matches 57; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

Db 1 evqlqsgaelvkgasvklscasgyftsywmhwkqshqskslwlgtrldpnsqtky 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 EVOLLESSEVKKPGSSVKVSCRASGSGFRSYNFNNVQAPGQGLEWMGGLIPMFGTANY 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ngkfkstltvdkssstymqltsedsavvyfars-y 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AQKFCGRVITTADESTATGYMELSLPSEDATVYVCAMPY 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
ID HV12_MOUSE STANDARD: PRT: 117 AA.
AC P01756;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE.

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RESULT 14
ID HV12_MOUSE STANDARD: PRT: 117 AA.
AC P06327;
DT DT 01-JAN-1988 (REL. 06, CREATED)
DT DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH58 A1/A4)
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; RODENTIA.
RN [1]
RP RN
RX MEDLINE: 8509340.
RA YANCOPOTLOS G-D, ALT F.W.;
RE CELL 40:271-281(1985).
DR EMBL; M13787; G456291; -
DE FIR; AC0039; HVM5A1.
DR HSSP: P01772; 1FOR.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 1 17 IG HEAVY CHAIN V REGION (VH58 A1/A4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12971 MW; A60F2B13 CPC32;

Query Match 45.8%; Score 435; DB 5; Length 117;
Best Local Similarity 58.8%; Pred. No. 7.25e+74;
Matches 57; Conservative 25; Mismatches 15; Indels 0; Gaps

Db 20 qvqlqsgpelvkqalvkvkscasgytfysdiavkrpqgglewivypqdskky 79
QY 1 EVOLLESESEVKKPCSSVKVSCPASGGSPFSYNFNWVPAPGGLIEMSGIIPMGITANY 50
      :|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 nekfkgtatldkssstaymqsltsensavyfca il6
      :|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ACKFGQVRITTADESTATGYMELSLRSEDATVYYCA 97

RESULT 15
ID HV13_MOUSE STANDARD: PRT: 117 AA.
AC P01757;
DT DT 21-JUL-1986 (REL. 01, CREATED)
DT DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (J3558).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; RODENTIA.
RN [1]
RP RN
RX MEDLINE: 80078170.
RA SCHILLING J, CLEVINGER R, DAVIE J M, HOWE L ;
RE NATURE 284:35-40(1980).
CC CC -!- THE SEQUENCES OF 10 HYPERIDOMA PROTEINS THAT ALSO BIND DEXTRAN
CC CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUP IN
CC CC THE D AND J SEGMENTS.
CC CC -!- THIS PROTEIN BINDS DEXTRAN.
DR DR FIR; A06242; MHMSJ5.
DR HSSP: P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 22 96
FT NON_TER 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;

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Db 1 evqlqsgpelykpaasvkmcskasytftdyymkvwkqshgkslewigdinpnngttsy 60
QY 1 EVQLLESGSEVKKPGSSVKVSCRASGGGFRSYNFWVRQAPQGGLWMGGIIPMEGTANY 60
Db 61 nqkfkgkatltvdksstaymqlnsltsedsavyyca----rd--r--yw-yfdwaaqt 111
QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAIVYTCAMPYPKHCSRGSWGDFWGGGT 120
Db 112 tvtvss 117
QY 121 LVTVSS 126

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Search completed: Tue Feb 24 07:15:44 1998  
 Job time : 19 secs.